

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:26:16 ; Search time 13.41 Seconds

(without alignments)
1108.748 Million cell updates/sec

Title: US-09-853-918-30

Perfect score: 1935

Sequence: 1 MADYLSGGTGVPEDELTA.....MSAQIEGTVHLSYERRLY 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1858	95.0	514	1	IMD1_HUMAN
2	1839	94.1	514	1	IMD1_MOUSE
3	1655	84.7	514	1	IMD2_MESAU
4	1653	84.6	514	1	IMD2_HUMAN
5	1640	83.9	514	1	IMD2_MOUSE
6	1348.5	69.0	537	1	IMDH_DROME
7	1245.5	63.7	524	1	IMH3_YEAST
8	1238.5	63.4	523	1	IMH2_YEAST
9	1233.5	63.1	523	1	IMH1_YEAST
10	1206.5	61.7	521	1	IMH3_CANAL
11	1095.5	56.0	514	1	IMDH_LEIDO
12	1094.5	56.0	512	1	IMDH_TRYBB
13	1016	52.0	502	1	IMH2_ARATH
14	1007.5	51.5	503	1	IMH1_ARATH
15	1001	51.2	454	1	IMH4_PNECA
16	691.5	35.4	403	1	IMH4_YEAST
17	649	33.2	490	1	IMDH_AOUAE
18	627.5	32.1	513	1	IMDH_BACSU
19	624.5	31.9	488	1	IMDH_ACTCA
20	613.5	31.4	521	1	IMDH_CHLVI
21	610.5	31.2	529	1	IMDH_MYCTU
22	601	30.7	404	1	IMDH_BORBU
23	600.5	30.7	404	1	IMDH_ECOCI
24	600.5	30.7	529	1	IMDH_MYCLE
25	587.5	30.1	487	1	IMDH_PASMU
26	586.5	30.0	488	1	IMDH_HAETN
27	577	29.5	492	1	IMDH_STRPY
28	574	29.4	481	1	IMDH_HELPY
29	572	29.3	481	1	IMDH_HELPJ
30	538	27.5	498	1	IMDH_RHTRR
31	505	25.8	496	1	IMDH_MERTA
32	491	25.1	485	1	IMDH_PYRAB
33	490.5	25.1	486	1	IMDH_PYRHO

34	490	25.1	485	1	IMDH_PYRFU
35	384.5	19.7	503	1	IMDH_TRIPO
36	348	17.8	479	1	Y143_MYCTU
37	344	17.6	345	1	GUAC_RAT
38	341	17.4	345	1	GUAC_HUMAN
39	331.5	17.0	356	1	GUAC_ASCSU
40	324	16.6	478	1	Y143_MYCLE
41	312	16.0	358	1	GUAC_ECOCI
42	306.5	15.7	346	1	GUAC_CAEBL
43	289.5	14.8	349	1	GUAC_BUCAT
44	188.5	9.6	375	1	Y110_MYCTU
45	168.5	8.6	375	1	Y110_MYCLE
46	118.5	6.1	238	1	HIS4_METVA
47	116.5	6.0	442	1	GLXD_RHME
48	115.5	5.9	311	1	PYRD_BACSU
49	114.5	5.9	313	1	PYRD_BACCL
50	109	5.6	1888	1	CALE_CHICK
51	106.5	5.4	163	1	Y22B_HAETN
52	106	5.4	360	1	ID12_HALNI
53	105.5	5.4	393	1	MDLB_PSEBU
54	105.5	5.4	572	1	DEY1_MOUSE
55	104	5.3	239	1	HIS4_METH
56	104	5.3	378	1	ZMPD_NEUCR
57	103.5	5.3	624	1	SERA_ARATH
58	103	5.2	393	1	LA2M_MYCSM
59	102.5	5.2	290	1	PYRD_SULSO
60	102	5.2	306	1	PYRD_MERTA
61	102	5.2	353	1	HAO3_HUMAN
62	101.5	5.2	569	1	URE1_BACRA
63	100.5	5.1	572	1	DEY1_MOUSE
64	100.5	5.1	252	1	DEY1_RAT
65	99.5	5.1	552	1	HIS6_RHOCA
66	99	5.1	238	1	HIS4_METTL
67	99	5.1	349	1	ID12_BACSU
68	98.5	5.0	244	1	PIRE_BACCL
69	98.5	5.0	354	1	CHVE_AGRAR
70	98.5	5.0	373	1	MDHM_CHLRE
71	98	5.0	352	1	HAO3_RAT
72	97	5.0	311	1	MDH_VIBCH
73	97	5.0	367	1	GOX2_ARATH
74	96	4.9	267	1	HIS6_MYCTU
75	96	4.9	367	1	GOX1_ARATH
76	96	4.9	463	1	MORD_RHME
77	95	4.9	369	1	GOX_SEPIOL
78	95	4.9	603	1	PURL_THEMA
79	94.5	4.8	253	1	PCRB_THEAC
80	94.5	4.8	449	1	ACCC_ECOCI
81	94.5	4.8	949	1	AHM6_ARATH
82	94.5	4.8	1556	1	GLTS_SYNF3
83	94	4.8	312	1	PYDB_ENTFA
84	94	4.8	351	1	HAO2_HUMAN
85	93.5	4.8	292	1	GTAB_BACSU
86	93.5	4.8	299	1	PYRD_ARCTU
87	93.5	4.8	1180	1	PYC2_YEAST
88	93	4.8	281	1	TRPA_COROL
89	93	4.8	306	1	PYRD_AOUAE
90	93	4.8	384	1	Y823_MYCLE
91	93	4.8	426	1	THCD_RHOER
92	93	4.8	609	1	Y4PA_RHISN
93	92.5	4.7	211	1	THIE_BACDH
94	92.5	4.7	342	1	ID12_RICCN
95	92.5	4.7	401	1	HUT1_CAUDR
96	92.5	4.7	416	1	ATTY_TRYOR
97	92.5	4.7	661	1	BAIH_EUSEP
98	92	4.7	261	1	THIG_MYCLE
99	92	4.7	264	1	THIG_XYLFA
100	91.5	4.7	444	1	Y808_CHLPN

ALIGNMENTS

RESULT 1

P42851 pyrococcus
P50097 titrichomo
O50591 mycobacteri
O92244 rattus norv
P36559 homo sapien
P27442 ascaris suu
O32912 mycobacteri
O16294 caenorhabdi
P15344 escherichia
P57300 buchnera ap
O50716 mycobacteri
O49721 mycobacteri
P05324 methanococ
O87392 rhizobium m
P25996 bacillus m
P46539 bacillus ca
P32018 gallus galli
O86223 haemophilus
O93he4 halobacteri
P20932 pseudomonas
O14194 homo sapien
O26531 methanobact
O01284 neurospora
O04130 arabidopsis
P21795 mycobacteri
O9ux04 sulfolobus
O58070 methanococ
O9nyq2 homo sapien
P41020 bacillus pa
P97427 mus musculu
O62950 rattus norv
O30724 rhodobacter
O50757 methanococ
P50740 bacillus su
P45535 bacillus ca
P54082 agrobacteri
O42686 chlamydomon
O07523 rattus norv
O9kut3 vibrio chol
O91rt9 arabidopsis
O55908 mycobacteri
O91rt80 arabidopsis
O52953 rhizobium m
P05414 spinacia ol
O95x03 thermotoga
O9hjh3 thermoplasma
P24182 escherichia
O9s2c9 arabidopsis
P55038 synechocyst
O47741 enterococcu
O9nyq3 homo sapien
O05852 b utp--ginc
O22513 archaeoglob
P33327 saccharomyc
P06562 corynebacte
O66451 aquifex aeo
O50049 mycobacteri
P43494 rhodococcus
P56610 rhizobium s
O9eyc8 bacillus ha
O92hm7 rickettsia
P58079 caluobacter
P33447 trypanosoma
P32330 eubacterium
O92b12 mycobacteri
O96f95 xyella fas
O92798 chlamydia p

IMDL_HUMAN
 ID IMDL_HUMAN STANDARD: PRT; 514 AA.
 AC P20839;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-1) (IMPDH 1).
 GN IMPDH1 OR IMPD1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=90203022; PubMed=1969416;
 RA Matsumeda Y., Ohno S., Kawasaki H., Konno Y., Weber G., Suzuki K.;
 RT "Two distinct cDNAs for human IMP dehydrogenase.";
 RL J. Biol. Chem. 265:5292-5295(1990).
 RN (2)
 RP CHARACTERIZATION.
 RX MEDLINE=95283610; PubMed=7763314;
 RA Hager P.W., Collart F.R., Huberman E., Mitchell B.S.;
 RT "Recombinant human inosine monophosphate dehydrogenase type I and type II proteins. Purification and characterization of inhibitor binding.";
 RL Biochem. Pharmacol. 49:1223-1329(1995).
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O = xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- TISSUE SPECIFICITY: IMP TYPE I IS THE MAIN SPECIES IN NORMAL LEUKOCYTES AND TYPE II PREDOMINATES OVER TYPE I IN THE TUMOR.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC
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 CC
 DR EMBL: J05272; AAA36114.1; ALT-SEQ.
 DR PIR: A35566; A35566.
 DR HSSP: P12268; 1B30.
 DR MIM: 146690;
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR010933; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS_2.
 DR Pfam: PF00478; IMPDH_C_1.
 DR Pfam: PF01574; IMPDH_N_1.
 DR SMART: SM00116; CBS_2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
 KW Multigene family; Repeat; CBS domain.
 FT DOMAIN 112 CBS 1.
 FT DOMAIN 177 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL)
 SQ SEQUENCE 514 AA; 55449 MW; 751303f8e9e21061 CRC64;

QY 1 MADYLLSGGTGYVPEDGLTAQQLFASADSLTYNDPILPGLFIDEVDELTSALTRKIT 60
 DB 1 MADYLLSGGTGYVPEDGLTAQQLFASADSLTYNDPILPGLFIDEVDELTSALTRKIT 60
 QY 61 LKTPPLISSPMDPTTEADMAIAMLKMGIGFIHNHNCPEQANVRKVKF----- 111
 DB 61 LKTPPLISSPMDPTTEADMAIAMLKMGIGFIHNHNCPEQANVRKVKFEDGEFTDPVY 120
 QY 112 ----- 111
 DB 121 LSPSHVGVLEAKMKHNGSGIPITETGTMGSKLVGIVTSRODFLAEKHDTLLSEVMT 180
 QY 112 ----- 111
 DB 181 PRIELVAPAGVTLKEANELLQSRKKGKLPYNDCELVAIIARTDLKKNRDYPLASKDS 240
 QY 112 -KLLCGAANGFREDKRYRLDLLTQAGVYIVYDSSQGSVYQIAVHYIKOKYPHLOYI 170
 DB 241 QKQLLCGAANGFREDKRYRLDLLTQAGVYIVYDSSQGSVYQIAVHYIKOKYPHLOYI 300
 QY 171 GGNVYTAQAQKNLIDAGVDGLRYGMCSSICITQEVMACGRPGTAIVRYAEYARRFGVP 230
 DB 301 GGNVYTAQAQKNLIDAGVDGLRYGMCSSICITQEVMACGRPGTAIVRYAEYARRFGVP 360
 QY 231 IADGSIQTVGHVYKALALGASTVMKSLAATTEAPGEFFSDGYRLKKRYGMSLDAM 290
 DB 361 IADGSIQTVGHVYKALALGASTVMKSLAATTEAPGEFFSDGYRLKKRYGMSLDAM 420
 QY 291 EKSSSOKRFESGDKVYKIAQGVSSIDQKSTQKRVPLVINGIHCODIGARSISVLR 350
 DB 421 EKSSSOKRFESGDKVYKIAQGVSSIDQKSTQKRVPLVINGIHCODIGARSISVLR 480
 QY 351 SMYSGELKFEKRTMSAQIEGCVHGLSHYEKRLY 384
 DB 481 SMYSGELKFEKRTMSAQIEGCVHGLSHYEKRLY 514

RESULT 2
 IMDL_MOUSE
 ID IMDL_MOUSE STANDARD: PRT; 514 AA.
 AC P50096;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 1 (EC 1.1.1.205) (IMP dehydrogenase 1) (IMPDH-1) (IMPDH 1).
 GN IMPDH1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukemia;
 RA Dayton J.S., Mitchell B.S.;
 RL Submitted (Aug-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O = xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC
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DR EMBL: U00978; AAA18285.1; -
 DR HSSP: P12268; 1B30.
 DR MGD: MGI:96567; Impdh1.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 DR Oxidoreductase: NAD: GMP biosynthesis; Purine biosynthesis;
 KM Multigene family; Repeat: CBS domain.
 FT DOMAIN 112 167 CBS 1.
 FT BINDING 177 232 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL).
 SQ SEQUENCE 514 AA; 55294 MW; B38AA2EB0EC64CE CRC64;

Query Match 94.1%; Score 1839; DB 1; Length 514;
 Best Local Similarity 72.8%; Pred. No. 3.9e-131;
 Matches 374; Conservative 6; Mismatches 4; Indels 130; Gaps 1;

QY 1 MADYLLSGTGYVPEDGLTAQOLFASADGLTYNDPILPGFIDFADDEVLTSLTKRTT 60
 DB 1 MADYLLSGTGYVPEDGLTAQOLFASADGLTYNDPILPGFIDFADDEVLTSLTKRTT 60
 QY 61 LKTPLLSPMDVTEADMAIAMAIMGIGFIHNCNTPFOANEVRKVKED----- 111
 DB 61 LKTPLLSPMDVTEADMAIAMAIMGIGFIHNCNTPFOANEVRKVKED----- 111
 QY 112 ----- 111
 DB 121 LSPSHVGVGLVLAQKHGFGSIPITATGTMSKLVGIVTSRIDFLAEKDHDTLLSEVMT 180
 QY 112 ----- 111
 DB 181 PRVELVVAAGVTLKANEILORSKKGKPIYNDDELVAIIARTDLKKNRDYPLASKDS 240
 QY 112 -KTLGGAAGVTRREDDKYRLDLTQAGVDVYVLDSSQGSNVYOIAMVHYIKOKYPHLYI 170
 DB 112 -KTLGGAAGVTRREDDKYRLDLTQAGVDVYVLDSSQGSNVYOIAMVHYIKOKYPHLYI 170
 QY 241 HKOLGGAAGVTRREDDKYRLDLTQAGVDVYVLDSSQGSNVYOIAMVHYIKOKYPHLYI 300
 DB 241 HKOLGGAAGVTRREDDKYRLDLTQAGVDVYVLDSSQGSNVYOIAMVHYIKOKYPHLYI 300
 QY 171 GGNVYTAAGAKNLLDAGVGLRVMGCGSICITQEVMACGRPGTAVVYVAEYARFEGVP 230
 DB 301 GGNVYTAAGAKNLLDAGVGLRVMGCGSICITQEVMACGRPGTAVVYVAEYARFEGVP 360
 QY 231 IIAADGIQVGHVVKALAGASTVVMGSLAATTEAEGEYFPFSDGRLTKRYMGSLDM 290
 DB 361 VIAADGIQVGHVVKALAGASTVVMGSLAATTEAEGEYFPFSDGRLTKRYMGSLDM 420
 QY 291 EKSSSSQKRYFSEGDVKVIAAGVSGSIQDKSGIQKFPVPLIAGIQGCCDIGARSLSVLR 350
 DB 421 EKSSSSQKRYFSEGDVKVIAAGVSGSIQDKSGIQKFPVPLIAGIQGCCDIGARSLSVLR 480
 QY 351 SMYSGELFEKRTMSAOIEGCVHGLHSTYERKLY 384
 DB 481 SMYSGELFEKRTMSAOIEGCVHGLHSTYERKLY 514
 RESULT 3
 ID2_MESAU STANDARD; PRT; 514 AA.
 AC P12269;
 DT 01-OCT-1989 (rel. 12, Created)
 DT 01-OCT-1989 (rel. 12, Last sequence update)
 DT 01-NOV-1997 (rel. 35, Last annotation update)
 DE Inosine 5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
 dehydrogenase 2) (IMPDH-II) (IMPD 2).

GN IMPDH2 OR IMPDH.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxId=10036;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 336-370.
 RX MEDLINE=89008491; PubMed=2902093;
 RA Collart F.R., Huderan E.;
 RT "Cloning and sequence analysis of the human and Chinese hamster
 RT Inosine-5'-monophosphate dehydrogenase cDNAs.";
 RL J. Biol. Chem. 263:15769-15772(1988).
 CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) =
 CC xanthosine 5'-phosphate + NADH.
 CC -!- PATHWAY: FIRST REACTION UNIT TO GMP BIOSYNTHESIS.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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DR EMBL: J04209; AAA36993.1; -
 DR PIR: B31997; B31997.
 DR HSSP: P12268; 1B30.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 DR Oxidoreductase: NAD: GMP biosynthesis; Purine biosynthesis;
 KM Multigene family; Repeat: CBS domain.
 FT DOMAIN 112 167 CBS 1.
 FT BINDING 177 232 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL).
 SQ SEQUENCE 514 AA; 55890 MW; 5FA0138FA41E8A02 CRC64;

Query Match 84.7%; Score 1655; DB 1; Length 514;
 Best Local Similarity 63.6%; Pred. No. 2.7e-117;
 Matches 327; Conservative 31; Mismatches 26; Indels 130; Gaps 1;

QY 1 MADYLLSGTGYVPEDGLTAQOLFASADGLTYNDPILPGFIDFADDEVLTSLTKRTT 60
 DB 1 MADYLLSGTGYVPEDGLTAQOLFASADGLTYNDPILPGFIDFADDEVLTSLTKRTT 60
 QY 61 LKTPLLSPMDVTEADMAIAMAIMGIGFIHNCNTPFOANEVRKVKED----- 111
 DB 61 LKTPLLSPMDVTEADMAIAMAIMGIGFIHNCNTPFOANEVRKVKED----- 111
 QY 112 ----- 111
 DB 121 LSPKRVDRVFEAKARHGFCGIPITDTGRMGRVGISSRIDFLKEEHDHFLIEIMT 180
 QY 112 ----- 111
 DB 181 KREDLVVAAGITLKANEILORSKKGKPIYNDDELVAIIARTDLKKNRDYPLASKDA 240
 QY 112 -KTLGGAAGVTRREDDKYRLDLTQAGVDVYVLDSSQGSNVYOIAMVHYIKOKYPHLYI 170

DB 241 KQOLCGAALGTHREDDKRYRLDILLALAGVYVLLDSQGSNIFQIMTKMKEXYPNLQVI 300
 QY 171 GGNVYTAQAOKNLIDACVDDL RVMGCGSICITQEVACGRPOGTAVYKVAEYARFGVP 230
 DB 301 GGNVYTAQAOKNLIDACVDDL RVMGCGSICITQEVACGRPOGTAVYKVAEYARFGVP 360
 QY 231 IADGGIGYGVHYKALALASTVMGSLAATTAPGEYFFSDGVRLKRYRGMSLDAM 290
 DB 361 VADGGIGYGVHYKALALASTVMGSLAATTAPGEYFFSDGVRLKRYRGMSLDAM 420
 QY 291 EKSSSOKRFESEGGDKYKIQVSGSIOGKSFVPTIAGIOHGCODIGARSLSVLR 350
 DB 421 DKHSSONRFFSEADKTKVQGVSGAVODKGSIHKEFVPILAGIQHSCODIGAKSLTQVR 480
 QY 351 SMWYSGELKFEKRTMSAOIEGVGSLHYEKRRLY 384
 DB 481 AMWYSGELKFEKRTMSAOIEGVGSLHYEKRRLY 514
 RESULT 4
 ID IM2_HUMAN STANDARD; PRT; 514 AA.
 AC P12268;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
 dehydrogenase 2) (IMPDH-II) (IMPD 2).
 GN IMPDH2 OR IMPD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=89008491; PubMed=2902093;
 RA Collart F.R., Huberman E.;
 RT "Cloning and sequence analysis of the human and Chinese hamster
 RT Inosine-5'-monophosphate dehydrogenase cDNAs.";
 RL J. Biol. Chem. 263:15769-15772(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=90203022; PubMed=1969416;
 RA Natsumeda Y., Ohno S., Kawasaki H., Konno Y., Weber G., Suzuki K.;
 RT "Two distinct cDNAs for human IMP dehydrogenase.";
 RL J. Biol. Chem. 265:5292-5295(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95091778; PubMed=7999076;
 RA Giesne D.A., Huberman E.;
 RT "Cloning and sequence of the human type II IMP dehydrogenase gene";
 RL Biochem. Biophys. Res. Commun. 205:537-544(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95204479; PubMed=7898627;
 RA Zimmermann A.G., Sychala J., Mitchell B.S.;
 RT "Characterization of the human Inosine-5'-monophosphate dehydrogenase
 RT type II gene.";
 RL J. Biol. Chem. 270:6808-6814(1995).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=95283610; PubMed=7763314;
 RA Hager P.W., Collart F.R., Huberman E., Mitchell B.S.;
 RT "Recombinant human Purification and characterization of Inhibitor
 RT binding.";
 RL Biochem. Pharmacol. 49:1323-1329(1995).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=99199217; PubMed=10097070;

RA Colby T.D., Vanderveen K., Strickler M.D., Markham G.D.,
 RA Goldstein B.M.;
 RT "Crystal structure of human type II inosine monophosphate
 RT dehydrogenase: implications for ligand binding and drug design";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:3531-3536(1999).
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- TISSUE SPECIFICITY: IMP TYPE I IS THE MAIN SPECIES IN NORMAL
 CC LEUKOCYTES AND TYPE II PREDOMINATES OVER TYPE I IN THE TUMOR.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: J04208; AAA36112.1; -;
 DR EMBL: L33842; AAA67054.1; -;
 DR EMBL: L39210; AAB70699.1; -;
 DR PIR: A31997; A31997.
 DR PIR: B35566; B35566.
 DR PDB: 1B30; 12-APR-99.
 DR MIM: 146691; -;
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
 KW Multigene family; Repeat; CBS domain; 3D-structure.
 FT DOMAIN 112 167 CBS 1.
 FT DOMAIN 177 232 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL).
 FT CONFLICT 190 191 AC -> RS (IN REF. 1).
 FT SEQUENCE 514 AA; 55805 MW; 876BEA0EC1DDBE9 CRC64;
 Query Match 84.6%; Score 1653; DB 1; Length 514;
 Best local Similarity 63.8%; Pred. No. 3,9e-117;
 Matches 328; Conservative 29; Mismatches 27; Indels 130; Gaps 1;
 QY 1 MADYLLISGTVYEDGELFAAQLFASADGLTYNDPLILPGFIDFIADVDLSALTRKIT 60
 DB 1 MADYLLISGTVYEDGELFAAQLFASADGLTYNDPLILPGFIDFIADVDLSALTRKIT 60
 QY 61 LKTPILSSPMDTYTEADMAIAMLGMGIGIFIHNCPEPOANVRKVKPPD----- 111
 DB 61 LKTPILSSPMDTYTEADMAIAMLGMGIGIFIHNCPEPOANVRKVKPPD----- 111
 QY 112 ----- 111
 DB 121 LSPKDRVRYFEAKAHGFCGIPITDTGRMGSRLVGISSROIDLKEEHDFLEIMT 180
 QY 112 ----- 111
 DB 181 KREDLVVAPAGITLKEANELLQSKKGLPIYNEDELVAIARTDLKKNRDPPLASKDA 240
 QY 112 -KTLGCAVGTREDDKRYRLDILLTQAGVDVYVLLDSQGSNIVQIAVHYIKQYPHLOVI 170


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Db      241 KRÖLLCGAIGTHEDDKRLDLAAGVVDVLDSSQNSISIPQIMKIKYKPNLQYI 300
Oy      171 GGNVYTAQAQAKLIDAGVDGLRVGMGCGSICITQEMVACGRPGQTAAYVVAEYARFGVP 230
Db      301 GGNVYTAQAQAKLIDAGVDGLRVGMGCGSICITQEVLAAGRQATVAVKVSSEYARFGVP 360
Oy      231 ITADGIGTGVHVAALAGASTVMGSLAATTEAPGEFFSDGVRLLKRYGMSLDAM 290
Db      361 VIADGIGTGVHVAALAGASTVMGSLAATTEAPGEFFSDGVRLLKRYGMSLDAM 420
Oy      291 EKSSSSQKRYFSEGDVKVIAQGVSSIDQKSIQKFPVLLAGIGHGCDIGARSLSVLR 350
Db      421 DKHLSSQNRFESEADKIKVAGGVSAVODKSGIHKFPVLLAGIGHGCDIGAKSLTQVR 480
Oy      351 SMVSGELKFEKRTMSAQIEGCVHGLHSYERKLY 384
Db      481 AMVSGELKFEKRTMSAQIEGCVHGLHSYERKLY 514

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RESULT 5

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IMD2_MOUSE STANDARD: PRT: 514 AA.
ID      01-MAR-1992 (Rel. 21, Created)
AC      P24547; 061734;
DT      01-MAR-1992 (Rel. 21, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
GN      IMPDH2 OR IMPDH.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      NCBI_TaxID=10090;
RP      [1]
RC      SEQUENCE FROM N.A.
RA      MEDLINE=91153661; PubMed=1671845;
RT      Tiedeman A.A., Smith J.M.;
RL      "Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase.";
RN      Gene 97:289-293(1991).
RP      [2]
RC      SEQUENCE FROM N.A. AND VARIANTS MYCOPHENOLIC ACID RESISTANT.
RA      TISSUE=Brain;
RT      MEDLINE=94153991; PubMed=7906545;
RT      Lightfoot T., Snyder F.F.;
RT      "Gene amplification and dual point mutations of mouse IMP
RT      dehydrogenase associated with cellular resistance to mycophenolic
RT      acid.";
RL      Biochim. Acta 1217:156-162(1994).
CC      -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC      OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC      OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
CC      CALICANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
CC      -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + H(2)O =
CC      xanthosine 5'-phosphate + NADH.
CC      -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC      -1- SUBUNIT: HOMOTETRAMER.
CC      -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC      GMP REDUCTASE.
CC      -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: M33934; AAA39311.1;
DR      EMBL: M98333; AAA20181.1;
DR      PIR: J70565; J70565.
DR      HSSP: P12268; 1B30.

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DR      MGD: MGI:109367; Impdh2.
DR      InterPro: IPR000644; CBS.
DR      InterPro: IPR001009; FMN enzyme.
DR      InterPro: IPR001093; IMP_DH_GMP_RED.
DR      Pfam: PF00571; CBS; 2.
DR      Pfam: PF00478; IMPDH_C; 1.
DR      Pfam: PF01574; IMPDH_N; 1.
DR      SMART: SM00116; CBS; 2.
DR      PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW      Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW      Multigene family; Repeat; CBS domain.
FT      DOMAIN 112 167
FT      DOMAIN 177 232
FT      BINDING 331 331
FT      BINDING 331 331
FT      VARIANT 333 333
FT      VARIANT 351 351
FT      VARIANT 351 351
FT      CONFLICT 483 483
FT      SEQUENCE 514 AA; 55785 MW; DSB6A5CSEBCC421 CRC64;

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Query Match 83.9%; Score 1640; DB 1; Length 514;
 Best Local Similarity 63.4%; Pred. No. 3.7e-116;
 Matches 326; Conservative 29; Mismatches 29; Indels 130; Gaps 1;

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Oy      1 MADYLIISGGTGVVPPDGLTAQOLFASADGLTYNDLILPGFIDFLADEVDLFSALTRKIT 60
Db      1 MADYLIISGGTGVVPPDGLTAQOLFASADGLTYNDLILPGFIDFLADEVDLFSALTRKIT 60
Oy      61 LKTPLISSPMDVTEDADMAIAMAALNGIGGIFIHNCNTPFQANVKKVKKFD----- 111
Db      61 LKTPLISSPMDVTEDADMAIAMAALNGIGGIFIHNCNTPFQANVKKVKKVKKFD----- 111
Oy      121 ISPKDRVDFEAKARHFGCGIPITDTGRMSRLVGISSRDIDELKEEHDHFLFEIWT 180
Db      121 ISPKDRVDFEAKARHFGCGIPITDTGRMSRLVGISSRDIDELKEEHDHFLFEIWT 180
Oy      112 ----- 111
Db      112 ----- 111
Oy      181 KREDLVVAPAGTYLKEANETLORSKKKRLPIYNDDELVAIITARDLKKRNDYPLASKDA 240
Db      181 KREDLVVAPAGTYLKEANETLORSKKKRLPIYNDDELVAIITARDLKKRNDYPLASKDA 240
Oy      112 -KTLGGAAGVTRDEDDKRLDLTQAGVDVIVLDSSQNSVYQIAMVHYIKQRYHLOVI 170
Db      112 -KTLGGAAGVTRDEDDKRLDLTQAGVDVIVLDSSQNSVYQIAMVHYIKQRYHLOVI 170
Oy      241 KRÖLLCGAIGTHEDDKYRLDLAAGVVDVLDSSQNSISIPQIMKIKYKPNLQYI 300
Db      241 KRÖLLCGAIGTHEDDKYRLDLAAGVVDVLDSSQNSISIPQIMKIKYKPNLQYI 300
Oy      171 GGNVYTAQAQAKLIDAGVDGLRVGMGCGSICITQEMVACGRPGQTAAYVVAEYARFGVP 230
Db      171 GGNVYTAQAQAKLIDAGVDGLRVGMGCGSICITQEMVACGRPGQTAAYVVAEYARFGVP 230
Oy      301 GGNVYTAQAQAKLIDAGVDGLRVGMGCGSICITQEVLAAGRQATVAVKVSSEYARFGVP 360
Db      301 GGNVYTAQAQAKLIDAGVDGLRVGMGCGSICITQEVLAAGRQATVAVKVSSEYARFGVP 360
Oy      231 ITADGIGTGVHVAALAGASTVMGSLAATTEAPGEFFSDGVRLLKRYGMSLDAM 290
Db      231 ITADGIGTGVHVAALAGASTVMGSLAATTEAPGEFFSDGVRLLKRYGMSLDAM 290
Oy      361 VIADGIGTGVHVAALAGASTVMGSLAATTEAPGEFFSDGVRLLKRYGMSLDAM 420
Db      361 VIADGIGTGVHVAALAGASTVMGSLAATTEAPGEFFSDGVRLLKRYGMSLDAM 420
Oy      291 EKSSSSQKRYFSEGDVKVIAQGVSSIDQKSIQKFPVLLAGIGHGCDIGARSLSVLR 350
Db      291 EKSSSSQKRYFSEGDVKVIAQGVSSIDQKSIQKFPVLLAGIGHGCDIGARSLSVLR 350
Oy      421 DKHLSSQNRFESEADKIKVAGGVSAVODKSGIHKFPVLLAGIGHGCDIGAKSLTQVR 480
Db      421 DKHLSSQNRFESEADKIKVAGGVSAVODKSGIHKFPVLLAGIGHGCDIGAKSLTQVR 480
Oy      351 SMVSGELKFEKRTMSAQIEGCVHGLHSYERKLY 384
Db      351 SMVSGELKFEKRTMSAQIEGCVHGLHSYERKLY 384
Oy      481 AMVSGELKFEKRTMSAQIEGCVHGLHSYERKLY 514
Db      481 AMVSGELKFEKRTMSAQIEGCVHGLHSYERKLY 514

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RESULT 6

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IMDH_DROME STANDARD: PRT: 537 AA.
ID      007152; 026455; 09W2R8;
AC      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE      dehydrogenase) (IMPDH) (Rasberry protein).
GN      RAS OR CG1799.

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QY 111 -----DKTLGCAAV 120
 Db 210 GINLEPTANAILEKSKKGLPIYNQAGELVAMIAFTDLKARSYPNASKSNQILLVGA1 269
 QY 121 GREDDEKRYDLITQAGVDVILDSOGNSYQIAMVHIKOKYIHLQVIGNVTAQA 180
 Db 270 GRSDEKARLALLVANGVDIILDSOGNSYQVEMIKYIKETPELOVIGNVTRAQA 329
 QY 181 KLIDAGVDGLRVGCGSICITQEVMAAGCPGQTAAYKVAARFPGPIIADGIGIOTV 240
 Db 330 KLIDAGVDGLRVGCGSICITQEVMAAGCPQATAYVQSTYAAQFGVPIADGIGIOTV 389
 QY 241 GHVYKALAGASTVMGSLAATPEAPEFPSPDVRILKRYKMGSLDAME----KSSSS 296
 Db 390 GHVYKALAGASTVMGSLAATPEAPEFPSPDVRILKRYKMGSLDAMEGDAKGAAM 449
 QY 297 OKRYSEGDVKYIAQGVSSIDDKSGIQKFPVYLLAGIOHGCQDIDGANSLSLRSMMSG 356
 Db 450 SKRYHNEMDKMKVAGVSGSIVDKGSVLYRPLRYLPCGLOHSCODIGANSINKLRMIYNG 509
 QY 357 ELKFEKRTMSAOIEGGVHGLHSYERKLY 384
 Db 510 QURFKRTHSAQIEGNGHGLSEYERKLF 537

RESULT 7
 ID IMH2_YEAST STANDARD: PRT: 524 AA.
 AC P50094:
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP dehydrogenase) (IMPDH) (IMPD).
 GN YML056C OR YML958.06C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Devlin K., Churcher C., Barrell B.G., Rajandream M.A.;
 RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIT OF GMP BIOSYNTHESIS.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC -----
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 CC -----
 CC EMBL: Z46729; CAA86719.1; -
 DR HSSP: P12268; I830.
 DR SGD: S0004520; YML056C.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 KM Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
 RL Putative biosynthesis; Multigene family; Repeat; CBS domain.
 FT DOMAIN 120 175 CBS 1.

FT DOMAIN 183 235 CBS 2.
 FT BINDING 336 336 IMP (POTENTIAL).
 SQ SEQUENCE 524 AA; 56394 MW; A73D1E4EE8AEAD9 CRC64;

Query Match 63.7%; Score 1245.5; DB 1; Length 524;
 Best Local Similarity 49.0%; Pred. No. 1.8e-86;
 Matches 248; Conservative 58; Mismatches 67; Indels 133; Gaps 3;

QY 12 YPEDGLTAQQLFASA--DGLTYNDFLLPGRIDPDAEVDLTSALTRTKTLTLPSSP 69
 Db 18 YSSKDLVQLMDSTRTGGLTYNDPLVGLVNPSSAVSLQTLTKTLTLNTPVSSP 77
 QY 70 MDVTADMAIYALMALMGIGIFTHNCTPEFQANEVRYKKFKFD-----111
 Db 78 MDVTADMAIYALMALMGIGIFTHNCTPEFQANEVRYKKFKFD-----111
 QY 112 -----111
 Db 138 VKMKRRKFGSGFPVTEDEKCPGLVGLVTSRDIQFLDEDSLIVSEVMTKNPVGIGIT 197
 QY 112 -----KTLGCAAVGT 122
 Db 198 LKEGNEILKQTKRGLLIVDNGNLVSMLSRADLKNQNPYLSKSAATTKOLLGAAIGT 257
 QY 123 REDDKYRLDLITQAGVDVILDSOGNSYQIAMVHIKOKYIHLQVIGNVTAQAQKN 182
 Db 256 IEADKERLRLVEAGLDVYILDSOGNSYFQLMKWKIKETPELITAGNVATEQAAN 317
 QY 183 LIDAGVDGLRVGCGSICITQEVMAAGCPQGTAVYKYAEVARRFGVPIIADGIGIOTVGH 242
 Db 318 LIAAGADGLRIQMGSGSICITQEVMAAGCPQGTAVYVNCQFANQGVPCMAQGVQNIQH 377
 QY 243 VKKALALAGASTVMGSLAATPEAPEFPSPDVRILKRYKMGSLDAMEKS----SSQK 298
 Db 378 IYKALALAGASTVMGSLAATPEAPEFPSPDVRILKRYKMGSLDAMEKSNKNAIST 437
 QY 299 RFSEGDVKYIAQGVSSIDDKSGIQKFPVYLLAGIOHGCQDIDGANSLSLRSMMSG 358
 Db 438 RFSESDSVLVAGVSGVAGVNDKSGIKRFLPYLXNGLOHSCQDIGESLTSLEKNVNGEV 497
 QY 359 KFEKRTMSAOIEGGVHGLHSYERKLY 384
 Db 498 REFRTASQALBGGVHGLHSYERKLY 523
 RESULT 8
 ID IMH2_YEAST STANDARD: PRT: 523 AA.
 AC P50095:
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP dehydrogenase) (IMPDH) (IMPD).
 GN YLR432W OR L9753.4.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Faveilo A., Fulton L., Gattung S., Greco T., Kirsten J.,
 RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
 RA Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
 RA Mardis E., Menezes S., Miller N., Nhan N., Pauley A., Peluso D.,
 RA Rifken L., Riles L., Tatch A., Trevisakis E., Vignati D.,
 RA Wilcox L., Wohlman P., Vaudin M., Watson R., Waterston R.,
 RL Submitted (Feb-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 xanthosine 5'-phosphate + NADH.

```

CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL: U21096; AAB67516.1; -.
DR HSSP: P12268; IB30.
DR SGD: S0004424; YLR432W.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
DR Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
KM Purine biosynthesis; Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT BINDING 182 234 CBS 2.
FT BINDING 335 335 IMP (POTENTIAL).
SQ SEQUENCE 523 AA; 56584 MW; A0C84C2527AAE6 CRC64;

Query Match 63.4%; Score 1238.5; DB 1; Length 523;
Best Local Similarity 48.6%; Pred. No. 6.1e-86;
Matches 244; Conservative 62; Mismatches 63; Indels 133; Gaps 3;

QY 16 DGLTAOOLFRS--ADGLTYNDFILPFGFIDFADVDLSALTRKTLKPLISSPMDTV 73
DB 21 DGLSVOLMLDSKIRGGLTYNDFILPGLVDFPSEVSLQTKLRNITLNPVSSPMDTV 80
QY 74 TEADMAIAMAIMGIGFIHNCPEFOANEVRKVKFD----- 111
DB 81 TESMAIFMALLGIGFIHNCPEQADVNRKKNENFINNPYISPTTYGEAKM 140
QY 112 ----- 111
DB 141 KEREGSGFVTEDEKENGKLMGIYVSRDIOFVEDNSLIVQDWTKNPVGAOGITLSEG 200
QY 112 -----KTLGGAAGTRED 126
DB 201 NEILKTKKKKKLLIVDNGMLVSMLSFTDLMKNONPFLASKSATTKQLCGAALGITDAD 260
QY 127 KYRDLDTLQAGVDVIVLDSOGNSVYOIAMVHYIKQYPLQVYIGVNVVAAQAKLIDA 186
DB 261 KERRLRLVEAGLVDVILDSOGNSIFGLNMKIKETFFPLEIITAGVNAIRREQANLAA 320
QY 187 GVGGLRVMGCGSICITQEVYMACGRPOGTIVYVAEYARFPVPIIADGSIQTVGHVKA 246
DB 321 GAGGLRIGMGSGSICITQEVYMACGRPOGTIVYVYCEAFANFGIICMADGVQNMIGHITKA 380
QY 247 LAIGASTVMMGSLLAATTEAPGEYFSDGVRLLKKYRGMGLDAMKS-----SSQKRYFS 302
DB 381 LAIGASTVMMGSLAGTTEAPGEYFODGRKLAYRGMGSLDAMOKTKGNASTRYFS 440
QY 303 EGDKVKIAQGVSGSIODKSGIOKFEVYPLGLIGIOGCGODIARSLSVLRSMYSGELFEK 362
DB 441 ESSSVLVAQGVSAVYDKSGIKKFIPLYLNGLOHSCODIGYKSLTLKENVQSGKAFER 500
QY 363 RTMSAOIEGGVHGLSHSEKRLY 384
DB 501 RTASAOLEGGVHMLSHSEKRLH 522

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RESULT 9
ID IMH1_YEAST STANDARD; PRT; 523 AA.
AC P38697;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Probable Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN PUR5 OR YHR216W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycaceae;
OC NCBI_TaxID=4932;
RX STRAIN=528BC / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favello A., Fulton L., Gatlung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
RA Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
RA Vaudin M.,
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RL Science 265:2077-2082(1994).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U00029; AAB6728.1; -.
DR PIR: S48997; S48997.
DR HSSP: P1268; IB30.
DR SGD: S0001259; PUR5.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KM Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KM Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT BINDING 182 234 CBS 2.
FT BINDING 335 335 IMP (POTENTIAL).
SQ SEQUENCE 523 AA; 56530 MW; 7CA3BEC11238906B9 CRC64;

Query Match 63.1%; Score 1233.5; DB 1; Length 523;
Best Local Similarity 48.6%; Pred. No. 1.5e-85;
Matches 244; Conservative 62; Mismatches 63; Indels 133; Gaps 3;

QY 16 DGLTAOOLFRS--ADGLTYNDFILPFGFIDFADVDLSALTRKTLKPLISSPMDTV 73
DB 21 DGLSVOLMLDSKIRGGLTYNDFILPGLVDFPSEVSLQTKLRNITLNPVSSPMDTV 80
QY 74 TEADMAIAMAIMGIGFIHNCPEFOANEVRKVKFD----- 111

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RP SEQUENCE FROM N.A.
RA MEDLINE-9107664; PubMed-1671039;
RX Wilson K.E., Collart F.R., Huberman E., Stringer J.R., Ullman B.;
RT "Amplification and molecular cloning of the IMP dehydrogenase gene of
  Leishmania donovani."
RL J. Biol. Chem. 266:1665-1671(1991).
CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
  OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
  OF CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
  xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
  GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC -----
DR EMBL: M55667; AAA29253.1; -
DR PIR: A38668; A38668.
DR HSSP: P12268; 1B30.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
  KM CBS domain. 110 165 CBS 1.
  FT DOMAIN 172 228 CBS 2.
  FT BINDING 327 327 IMP (POTENTIAL).
  SQ SEQUENCE 514 AA; 55551 MW; E251FC1362D0E5 CRC64;

Query Match 56.0%; Score 1095.5; DB 1; Length 514;
Best Local Similarity 44.0%; Pred. No. 3.5e-75;
Matches 219; Conservative 62; Mismatches 88; Indels 129; Gaps 3;

QY 15 EDELTAQQLFASADGLTYNDFLLPGRIDFIADENVDTLSLTRKITLTKTLPSSPMDTVT 74
DB 14 KDCETAELF-RGDGLTYNDFLLPGRIDFGADVNISGQFTKRIRLHPVSSPMDTIT 72
QY 75 EADMAIAMLGSGICFIHNCPEFOANEVRYKKF----- 110
DB 73 ENEMATMALMGSGVGLHNNCTYEROVEMKSKATRNCTISRPKSVPTPTISNIRIK 132
QY 111 ----- 110
DB 133 EEKIGSIIIVTENGDPHGKLLGIVCTKIDIDYVANKDTPVSAVMTBREKMTVERAPIQLEE 192
QY 111 -----DKT--LLCGAANGREDD 126
DB 193 AMDVLRNRYGLPIVNEDEVNLCRRDAVARADYPHSTLDKSGRLTCAATSTRPED 252
QY 127 KYRLDLITQAGVDVIVLDSQGSNSVQIAMVHYIKOKYPHLOVIGGVVTAQAOKNLIDA 186
DB 253 KRVVALADVGVIVLDSQGSNTYQIAFIKVKKSTPHLEVVAGNVVTDQDAKNLIDA 312
QY 187 GVDGLRVGKCGSICITQEVYMACGPGGTAVVVAEYARREGVPIIADGCIQTGVHVKVA 246
DB 313 GADGIRIGKMGSGICITQEVYMACGPGGTAVVVAEYARREGVPIIADGCIQTGVHVKVA 246
QY 247 LAIGASTVMMGSLAATTAEPGEYFSDGVRLKKYKMGSLDAMESSSSQKRYFSEGDK 306
DB 247 LAIGASTVMMGSLAATTAEPGEYFSDGVRLKKYKMGSLDAMESSSSQKRYFSEGDK 306

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DB 373 LAIGANCMALMGSLGTTPEFFKGVRLKYKMGSLDAMESSQKESGKRYLSENERA 432
QY 307 VKIAGVSGSIDRKSIOKGFVPLVIGIOHCODIGARSLSVSMYSSEGLFEKRTMS 366
DB 433 VQVAGSGSNVVDKSGAIAKIAVYVSGLDQSNADIGESIDALREKMYAGVLFSSRSP 492
QY 367 AOTEGGVHGLHSTYKRLY 384
DB 493 AOGEGGVHSLHSTYKRLF 510

RESULT 12
ID IMPDH_TRYB STANDARD; PRT; 512 AA.
AC P50098;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
  dehydrogenase) (IMPDH) (IMPD).
OS Trypanosoma brucei brucei.
OC Eukaryota; Euzoaria; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-EATRO 164 / ISTAT 1.7;
RX MEDLINE-95050714; PubMed-7961861;
RA Wilson K., Berens R.L., Sifri C.D., Ullman B.;
RT "Amplification of the inosinate dehydrogenase gene in Trypanosoma
  brucei gambiense due to an increase in chromosome copy number."
RL J. Biol. Chem. 269:28979-28987(1994).
CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
  OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
  OF CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
  xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
  GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M97794; AAB46420.1; -
DR HSSP: P12268; 1B30.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
  KM CBS domain. 108 163 CBS 1.
  FT DOMAIN 170 226 CBS 2.
  FT BINDING 325 325 IMP (POTENTIAL).
  SQ SEQUENCE 512 AA; 55708 MW; 1A86C46AE445045 CRC64;

Query Match 56.0%; Score 1094.5; DB 1; Length 512;
Best Local Similarity 44.1%; Pred. No. 4.1e-75;
Matches 219; Conservative 66; Mismatches 83; Indels 129; Gaps 3;

QY 16 DGLTAQQLFASADGLTYNDFLLPGRIDFIADENVDTLSLTRKITLTKTLPSSPMDTVT 75
DB 16 DGLTAQQLFASADGLTYNDFLLPGRIDFIADENVDTLSLTRKITLTKTLPSSPMDTVT 75

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Db 13 DGTAAELF-SQDLSFNDPFIILPGFIDFSSKVNVSQFTKILLHLPLVSSPMDVTYE 71
Qy 76 ADMAIAMLGMGIGFIHNCIPEFOANFVRKYKF----- 110
Db 72 SSMAKAMLMGIGIVIHNCIPEFOANFVRKYKF----- 131
Qy 111 -----DKT----- 110
Db 132 EKGISGILVTEGGKYDKGLLIGVCTKIDIFVKDASAPVSYMTRENTVERPIKLEEA 191
Qy 111 -----DKT----- 110
Db 192 MDVLRNRHGYLPVLNDEDEVVCLSRDAAVARDYPNSSLDNRHGLLCAATSTREADK 251
Qy 128 YRLDILTAGVYVYLDSSQNSVYQIAMVHYIKOKYPHLOYIGGNNVTAQAKULIADG 187
Db 252 GRVAALSRAGIDVLVDSSQNTYIYQSFIRKVKTYPHLEVAGNNVTOQAKMLIDNG 311
Qy 188 VDLGVNMGCGSICITQEVMACGRPOGTAVYKVAEYARFVPIADGIGIOTGVHVRAL 247
Db 312 ADSLRIGMGSSICITQEVMACGRPOGTAVYKVAEYARFVPIADGIGIOTGVHVRAL 371
Qy 248 ALGASTVMGSLAATTAPEGFYFSDGVRLKTRGMSLDAMEKSSSSOKRYESEGRV 307
Db 372 AVGANVAMLGIMAGTSETPEYEFKDMRLKGYRGMSIDAMLQGRESGRKYLESENTL 431
Qy 308 KIAQVSGSIDDKGSIQKQFVPLINGIOHGGODIGARSISVLRSMWYSGELKFEKRTMSA 367
Db 432 QVAGQVAGAVLDKGSVLLKLAIIHKGLQOASODIGEVSFDAIRKVEYEGVLFNRTTLA 491
Qy 368 QIEGGVHGLHSEYKRLY 384
Db 492 QSEGAVHSLHMYERKLF 508

RESULT 13
IMH2_ARATH STANDARD: PRT: 502 AA.
AC 09SA34:
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH).
GN AT1G16350 OR F309.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV. COLUMBIA.
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gali J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huitzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Miltschew J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley B.I.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uteback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana."
RL Nature 408:816-820(2000).

```

```

CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H2O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 1 CBS DOMAIN.
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CC
DR EMBL: AC006341; AAC34687.1; -.
DR HSSP: P12268; 1B30.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00478; IMPDH_C.1.
DR Pfam: PF01574; IMPDH_N.1.
DR PROSITE: PS00487; IMP_DH_GMP_RED.1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain.
FT DOMAIN 167 219 CBS.
FT BINDING 321 321 IMP (POTENTIAL).
SO SEQUENCE 502 AA; 54051 MW; FB87DB4160818310 CRC64;

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Query Match 52.0%; Score 1016; DB 1; Length 502;
Best local similarity 42.0%; Pred. No. 3,2e-69;
Matches 210; Conservative 61; Mismatches 97; Indels 132; Gaps 2;

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Qy 15 EDGLTAQQLFASADGLTYNDFLLPGFIDFIDAEVDLSATLTKTLKTPLISSPMDVTY 74
Db 5 EDGFSAEKLFSGQSYTYVDVFLPHFIDFSTDAVSLSTRKRVPLSIPCVASPMDTVS 64
Qy 75 EADMAIAMLGMGIGFIHNCIPEFOANFVRKYKF----- 110
Db 65 ESHMAAAMALGGIGIVIHNCIPEFOANFVRKYKF----- 124
Qy 111 -----DKT----- 110
Db 125 PSSFVFSQGTGLTPKLLGLGYSKSEMSMKDQKEVKIYDYKSCENKDYVPMIDIDK 184
Qy 111 -----DKT----- 124
Db 185 IEAVLEDKQGFVLEKEGEFVNVVTKDVERVKGYPKLSQTVGADKKMMVGAALGTRE 244
Qy 125 DDKYRLDILTAGVYVYLDSSQNSVYQIAMVHYIKOKYPHLOYIGGNNVTAQAKULI 184
Db 245 SKERLEHLVKNAGANVYLDSSQNSIYQLEIKYKVTPELDVGVGNVYMYQAEMLI 304
Qy 185 DAGVGLLRVGMCGSICITQEVMACGRPOGTAVYKVAEYARFVPIADGIGIOTGVHVR 244
Db 305 KAGVGLLRVGMCGSICITQEVMACGRPOGTAVYKVAEYARFVPIADGIGIOTGVHVR 364
Qy 245 KALAGASTVMGSLAATTAPEGFYFSDGVRLKTRGMSLDAMEKSSSSOKRYESEGR 304
Db 365 KALVYAGASTVMGSLAATTAPEGFYFSDGVRLKTRGMSLDAMEKSSSSOKRYESEGR 422
Qy 305 DKVKTAGVSGSIDDKGSIQKQFVPLINGIOHGGODIGARSISVLRSMWYSGELKFEKRT 364
Db 423 AKLKTAGVAGVADKGSILFIPYTHMAVYKOGFODLGLASSLOSARELLRNTLTLEART 482
Qy 365 MSAQIEGGVHGLHSEYKRLY 384
Db 483 GNAQIEGGVHGLHSEYKRSF 502

RESULT 14

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IMH1_ARATH STANDARD; PRT; 503 AA.
ID IMH1_ARATH
AC P47996;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
denhydrogenase) (IMPDH) (IMPD).
GN IMPDH OR AT1G9470 OR TBK14.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.
ON NCBI_TaxID=3702;
RX MEDLINE-97045815; PubMed-8890737;
RC STRAIN=CV. COLUMBIA;
RA Collart F.R., Ostlund J., Trent J., Olsen G.J., Huberman E.;
RT Cloning and characterization of the gene encoding IMP dehydrogenase
from Arabidopsis thaliana.";
RL Gene 174:217-220(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE-21016719; PubMed-11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,
RA Dunn P., Egan P., Feldlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lanz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malet A., Marzilli A.,
RA Miltischer J., Miranda M., Nguyen M., Niemann W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana".
RL Nature 408:816-820(2000).
CC -I- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
xanthosine 5'-phosphate + NADH.
CC -I- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -I- SIMILARITY: NO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
GMP REDUCTASE.
CC -I- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L34684; AAB41940.1; -
DR EMBL: AC007202; AAD30229.1; -
DR HSSP: P12268; I830.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR01093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS_1.
DR Pfam: PF00478; IMPDH_C_1.
DR Pfam: PF01574; IMPDH_N_1.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain.
FT BINDING 322 322 IMP (POTENTIAL).

SQ SEQUENCE 503 AA; 54194 MW; ADDDAF9C3A697A9A CRC64;
Query Match 51.5%; Score 1007.5; DB 1; Length 503;
Best Local Similarity 42.1%; Pred. No. 1.4e-68;
Matches 211; Conservative 62; Mismatches 95; Indels 133; Gaps 4;
QY 15 EDGTRAOQLFASADGLTYNDLFLPGFIDFADEVDTLSATFRKTLKPLISSPMDTYT 74
DB 5 EDGFPADKLFQAQGYSTYTDVIFLPFIDFSTDAVSLSTRLSRPVLSIPCVSPMDTVS 64
QY 75 EADMAIAMLMGIGIRHNC-----TFEFO----- 100
DB 65 ESHMAAAMSLGIGIVHNCIGIAAQSIIROAKSLKHPIASDAGVFPFEYETTSIDAFG 124
QY 101 ----- 100
DB 125 PSSFVFEOTGTYTTRKLLGYTKSQMKRMYEQREMKIYDYWKSCDSSDYCVPEIDE 184
QY 101 -----ANEVRKKKFDK-----LLGAAVGT 123
DB 185 KLEFVLEDKQKGFVLERDEYVNVYTKDIDQVKGYPKSGGTGVPDGEVMVGAALGT 244
QY 124 EDDKTRLDLITQADVIVYLDSSQNSVYQIAMVHFKQYRPHLOYTGNNVTAQAQKL 183
DB 245 ESKPERLEHVVNVAVAVVLDSSQNSIYOLEIKIKVKKTYELDIGNVVTVQAQKL 304
QY 184 IDAGVGLRVGKSGSICITQEFVACRGROGAVVAVVAVARFPGVPIADGIGTGVHV 243
DB 305 IDAGVGLRVGKSGSICITQEFVACRGROGAVVAVVAVARFPGVPIADGIGTGVHV 364
QY 244 VKALAGASTVMVMSLLAATTEAPGEYFSDGRLKRYKMGSLDAMEKSSSRKRYFE 303
DB 365 VKALVGLASTVMVMSLLAATTEAPGEYFSDGRLKRYKMGSLDAMEKSSSRKRYFE 422
QY 304 GDRVKTACGVSSGIDQKSGIOKFPVPLINGIOHGCDDIARSLSVLRSMYSGELAKFER 363
DB 423 QTRKLKIAQGVAVVADKGVSLKIPYTHAVKQGFODLASSLSQASHGLRSLNLRLEAR 482
QY 364 TMSAQTEGVGHGLSYEKRLY 384
DB 483 TGAQVGEVGHGLSYEKRSF 503
RESULT 15
ID IMH1_PNECA STANDARD; PRT; 454 AA.
AC 012658;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPD).
GN GNA1.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-97135213; PubMed-8980752;
RA O'Gara M.J., Lee C.H., Weinberg G.A., Nott J.M., Queener S.F.;
RT "IMP dehydrogenase from Pneumocystis carinii as a potential drug
target".
RL Antimicrob. Agents Chemother. 41:40-48(1997).
CC -I- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
xanthosine 5'-phosphate + NADH.
CC -I- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -I- SIMILARITY: NO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
GMP REDUCTASE.
CC -I- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: U42442; AAA97462.1; -
 DR HSSP: P12268; 1B30.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 KM Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
 KM CBS domain.
 FT DOMAIN 47 102 CBS 1.
 FT BINDING 109 163 CBS 2.
 FT BINDING 263 263 IMP (BY SIMILARITY).
 SQ SEQUENCE 454 AA; 49522 MW; 5E4B64426A730947 CRC64;

Query Match 51.2%; Score 1001; DB 1; Length 454;
 Best Local Similarity 44.8%; Pred. No. 3.9e-68;
 Matches 203; Conservative 52; Mismatches 64; Indels 134; Gaps 2;

OY 66 ISSPDVTYADMAIAMLGSGIFTHNCTPEFOANEYKVKFD----- 111
 DB 1 MSSPDVTYESDMAINLALGIGIVHNCTEEOETEMVRKVKFENGFTSPYLSLNH 60
 OY 112 ----- 111
 DB 61 RVRDVRRIKEELGFGSGIPTFTGOLNKLGIIVTSRDIOFNHNDSEFLSEVITKDLVTGS 120
 OY 112 -----KTLGCA 118
 DB 121 EGIRLEANEILRSCKKGLPIVDEKGNLTALLSRDLKKNLHFLASKLPSPKOLICQ 180
 OY 119 AVGTREDDKYRLDLTQAGVDVIVLSSGNSVYOIAMVHYTKOKYPHLOITGVNTAA 178
 DB 181 AVGTREDDKIRLKHVEAGLDIVLSSGNSIYOIMKMKKKEPNLEIAGNVVTR 240
 OY 179 QAKNLIDAGVDGLRYGMSGICITQEVMAACGRPGGTANYYKAEVARRGVPLIADGIG 238
 DB 241 QANLISAGADALRVGMSGISICITQELMAVGRPOATAVAYAVSEASKGVPLIADGIE 300
 OY 239 TVGHVKALALGASTVVMGSLAATTEAPGEFFSDVGLTKYRGMSIDAMEKSSSQK 298
 DB 301 NIGHITKALALGASAVMMGNLAGITTESRGORYRRGQGLKSTKRGMSIDAMEHLSGRKK 360
 OY 299 -----RYFSEGDVKVIAQVSGSIQDKSGIQKEFVYPLIAGIOHCQDIGARSLSVLR 351
 DB 361 GDNAASSRYFGADITRVAGVSGSVIDKSGSLHVVYPLRYLGTQHSLODIOGNLTLEKK 420
 OY 352 MMYSGLKFEKRTMSAQITGCVGHLSHYEKRLX 384
 DB 421 QVKEKNIRFEFRTVASQLGKGNVHGDSYOKKL 453

RESULT 16
 IMH4_YEAST
 ID IMH4_YEAST STANDARD: PRT: 403 AA.
 AC P39567;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE putative inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
 dehydrogenase) (IMPDH) (IMPD).
 GN YAR073W OR FUN63.
 OS Saccharomyces cerevisiae (Baker's yeast).

CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 CC NCBI_TaxID:4932;
 OX NCBI_TaxID:4932;
 RN RP
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=95249563; PubMed=7731988;
 RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
 RA Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
 RA Storms R.K.,
 RT "the nucleotide sequence of chromosome I from Saccharomyces
 RT cerevisiae".
 RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.

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CC EMBL: L28920; AAC09509.1; -
 DR HSSP: P12268; 1B30.
 DR SGD: S0000095; YAR073W.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 KM Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
 KM Purine biosynthesis; Multigene family; Repeat; CBS domain.
 FT DOMAIN 119 174 CBS 1.
 FT BINDING 182 235 CBS 2.
 FT BINDING 335 335 IMP (POTENTIAL).
 SQ SEQUENCE 403 AA; 44386 MW; FEBC13E46D5DIEDD CRC64;

Query Match 35.4%; Score 691.5; DB 1; Length 403;
 Best Local Similarity 41.2%; Pred. No. 6.6e-45;
 Matches 145; Conservative 35; Mismatches 43; Indels 129; Gaps 2;

OY 16 DGLTNOQLFAS--ADGLVYNDELILPGFTDFIADVDLTSALTRKTLTKPLISSPMDTV 73
 DB 21 DGLTNOQLDLSKIRGGLANDFLILGLVDFASSEVSQTKLRTNITLPIVSSPMDTV 80
 OY 74 TEADVAIAMLALGSGIGIFTHNCTPEFOANEYKVKFD----- 111
 DB 81 TESEMATFALLDLDIGIFTHNCTPEDQADMRVRVNYENGFINNIVISPTTVEAKSM 140
 OY 112 ----- 111
 DB 141 KEKYGAFGPVYADGKRNALVGATISRDIQFVEDNSLIVQDMKNPVTYGAQGITLSEG 200
 OY 112 -----KTLGCAANGTRED 126
 DB 201 NEILKIKKRGILLVYDEKGNLVSMLSRPDLKKNQYPLASKAANTKOLMGASISGTMDAD 260
 OY 127 KYRLDLTQAGVDVIVLSSGNSVYOIAMVHYTKOKYPHLOITGVNTAAQANLIDA 186
 DB 261 KERLRILVYAGLDVIVLSSGNSIFOLMIMIKETPTPDELITGVNTKQANLIDA 320
 OY 187 VDGSLRVGMSGISICITQEVMAACGRPGGTAVYKVAEYARRGVPLIADGIG 238
 DB 321 GADGLRIGMGTSICITQKVMACGRPGGTAVYVCEFAFNOFGVPCMDAGVQ 372

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RESULT 17
IDMH_AOUAE STANDARD: PRT; 490 AA.
AC 067820;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DN dehydrogenase) (IMPDH) (IMPD).
GN CUAB OR AQ_2023.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5.
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIOUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL: AE000768; AAC07779.1; -.
DR HSSP: P50099; 1ZFJ.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; PMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS_2.
DR Pfam: PF00478; IMPDH_C_1.
DR Pfam: PF01574; IMPDH_N_1.
DR SMART: SM00116; CBS_2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT DOMAIN 93 146 CBS 1.
FT DOMAIN 156 210 CBS 2.
FT BINDING 309 309 IMP (POTENTIAL).
SQ SEQUENCE 490 AA; 53400 MW; 66605CDBB8348CE4 CRC64;

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Query Match 33.2%; Score 649; DB 1; Length 490;
Best Local Similarity 33.2%; Pred. No. 1.3e-41;
Matches 157; Conservative 62; Mismatches 122; Indels 132; Gaps 3;

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OY 28 DGLTYNDLILPGFIDFIADVDLTSALRKTKLPPLISSPMDVTVDADMAIAMLG 87
OY :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 10 EGLTFDVLVLPQYSEVLPHPEVDVSTYLTFRKIKLIPISANDTVEARLAIAREGG 69
OY :||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 88 IGTIHNCPEPQANEVRYKKKFKDKLL----- 115
OY :||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 70 IGIHNNLPKQAEVEKKKSGMIINPVTKPDTRYKALDIMAKYKISGVVDE 129
OY :||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 116 ----- 115
DB 130 EKKLIGLITNRDLRTFKPEDYSKPVSEPMKENTLTAPEGITLDEADELFRKTKIKLPI 189

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OY 116 -----CGAAYGTREDDXRYRLDLLTQACVDYI 141
DB 190 VDKEGKIKGLITIKDIIVKRRKKYPNACKDELGRLRVGAAGVGETLDRVAALVEAGVDYI 249
OY 142 VLDSOGNSVYQIAMVHYTKOKYPLQVIGGNVYTAQAKNLIDAGVDGLRGMCGSGIC 201
OY :||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 250 VDTAFGHSKRVLETETEKIKANPEVDVLAGNAVTEGTRKALEADADVKYGVGPGSIC 309
OY 202 IPDEVACGRPOGTAVYKYAEVARRPVPILADGGIQTGFVGHVYKALALASVYMMGSLIA 261
DB 310 TTRIVAGVGPQLTALMEANSAAREVDITPIADGIRYSGDIYKALAAASVAMIGNLIA 369
OY 262 ATTEADGEYFFSDVRLKRYRCGSLDAMEKSSSQKRYFSEGDYVYKIAQVSGSIQDKG 321
DB 370 GTEADPGETIYVGGRAYKYVRCGMSLGAMSSRLSD-RYGOEKMEKFEVPEGIEGRVYRG 428
OY 322 STOKFPYPIIAGIOHCODIGASLSVLSSMMYSGELKFEKRMASQIIGVYH 374
DB 429 KIADVYVQLVGLRSGMGYVGARNIKELD-----KAKFVRLTWAGYRESHVH 476

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RESULT 18
IDMH_BACSU STANDARD: PRT; 513 AA.
AC P21879;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD) (Superoxide-inducible protein 12)
DE (S0112).
GN GUAB OR GNAB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91067483; PubMed=1979163;
RA Kanazaki N., Miyagawa K.I.;
RT "Nucleotide sequence of the Bacillus subtilis IMP dehydrogenase
RL gene."
RL Nucleic Acids Res. 18:6710-6710(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin."
RL DNA Res. 1:1-14(1994).
RN [3]
RP SEQUENCE OF 1-25.
RC STRAIN=ISS8.
RX MEDLINE=97443988; PubMed=9298659;
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
RA Hecker M.;
RT "First steps from a two-dimensional protein index towards a response-
RT regulation map for Bacillus subtilis."
RT Electrophoresis 18:1451-1463(1997).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIOUE TO GMP BIOSYNTHESIS.
CC -1- INDUCTION: BY SUPEROXIDE.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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OY 264 TEABGEFFSDGVRLLKRYRGMSLDAMEKSSSQKRYFE---GDKVYIAQVSGSIQDK 320
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 366 EEAAGEVEFFQGRYRKAYRCGMSLGAAGAGRTGSAFRFQDSKAGAEKLVPEGIGRVPYK 425
OY 321 GSIOKFPYPIYIAGIOHGCODIGARSLSVLRSMATSGELKEFKRMSAQIEGVH 374
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 426 GPMGNIVHQMGGILRSSMGYTGSAVIEDLRQ-----NAKFEVKITTSAGMSSESHV 474

RESULT 20
IMDH_CHLVT
ID IMDH_CHLVT STANDARD; PRT; 521 AA.
AC 050316;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
  dehydrogenase) (IMPDH) (IMPD).
GN GUA.
OS Chlorobium vibrioforme.
OC Bacteria; Green sulfur bacteria; Chlorobium.
ON NCBI_TaxId=1098;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F. THIOSULFOTROPHILUM NCIB 8327;
RA Petersen B.L., Moeller M.G., Stummann B.M., Henningsen K.W.;
RT Clustering of genes with function in the biosynthesis of
  bacteriochlorophyll and heme in the green sulfur bacterium Chlorobium
  vibrioforme."
RT Hereditas 125:93-96(1996).
RL
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
  xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
  GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL: 283933; CAB06303.1; -.
DR HSSP: PA9058; 1EEP.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KM Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
  CBS domain.
FT DOMAIN 118 176 CBS 1.
FT DOMAIN 184 237 CBS 2.
FT BINDING 336 336 IMP (POTENTIAL).
SQ SEQUENCE 521 AA; 56627 MW; 0065FCCBC182815A CRC64;

Query Match 31.4%; Score 613.5; DR 1; Length 521;
Best Local Similarity 30.8%; Pred. No. 6, 6e-39;
Matches 147; Conservative 64; Mismatches 130; Indels 137; Gaps 4;
OY 28 DGLTYNDFLLPFIADVDLTSLTRKILTKPLISSPMDVTEADMAIAMLGMG 87
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 35 DALTFPDVLLPAVYANVLPRKETYVKSRYTNIEVNLPLVSAANDTYTEAFALAIARAGS 94

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OY 88 IGFHNHCPEFOANEYRVKVKFFDKTL----- 115
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 95 IGIHKRLSIDVOARHVAKVRFESGIIIRNPITLFEDATIOEAIDMLRHSIGIPVER 154
OY 116 ----- 115
Db 155 PRPEGCLLKGIYVNDLRMTTSSNEKITITITDITAOEDIDLLAEELMOKNIEKL 214
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 116 ----- 115
Db 215 LVIDEBCYLKGLTFKDIQKRCQPDACKMDHRLNVAAGVAVGIRSNITFRVDLVAEAGVD 274
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 140 VIVLDSQGNVYOIAMVHYIKOKYPHLOYIGNVVTAQAKLIDAGVDGLRVGKCGS 199
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 275 VVAVDPAHNGSQAVLDMVATIKERPELEVIAGNVATPEAVRDLVRAADAVVGIGPGS 334
OY 200 ICTTOEMACGPRGQAVYVAEYARFRFVPIIADGIGTGVHVVALGASTVMGSI 259
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 335 ICTRVVAGVMPOLTRAINCAEAKATPTPIADGIRKISGDISKALAGADPTVMGSI 394
OY 260 LAATTEAPGEFFSDGVRLLKRYRGMSLDAMEKSSSQKRYFESEGD---KVKIAQVSGS 316
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 395 FACTDESPEGETILYEGRRFAYRGMSLGAHMSPESSDRYFQDASAEKTKYVEGIEGR 454
OY 317 IQDKSIQKFPYPIYIAGIOHGCODIGARSLSVLRSMATSGELKEFKRMSAQIEGVH 374
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 455 IPR-PLDEVVYOLIGLSKMSGCGVKNTIELK-----NFRFVITTSAGLRESHPH 506
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 21
IMDH_MYCTU
ID IMDH_MYCTU STANDARD; PRT; 529 AA.
AC 050715;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
  dehydrogenase) (IMPDH) (IMPD).
GN GUA. OR RV3411C OR MT3519 OR MTCY78.17.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
  Mycobacteriales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxId=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
  Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala R.,
  Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
  Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,
  Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
  Oliver S., Osborne J., Quail M.A., Raftery M.A., Rogers J.,
  Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
  Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
  RA "Deciphering the biology of Mycobacterium tuberculosis from the
  RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
  RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
  RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
  RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
  RA Bishai W.;
  RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
  RT laboratory strains."
  RT Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
  RL -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
    xanthosine 5'-phosphate + NADH.
  CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
  CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

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CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL: Z77165; CAB01012.1; -.
DR EMBL: AE007157; AKK47857.1; -.
DR HSSP: P12268; 1B30.
DR TIGR: MT3519; -.
DR TruncatList: rv3411c; -.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT BINDING 341 341 IMP (POTENTIAL).
SQ SEQUENCE 529 AA; 54867 MW; 689A/C7C53993C0A CRC64;

Query Match 31.2%; Score 610.5; DB 1; Length 529;
Best Local Similarity 32.0%; Pred. No. 1,1e-38;
Matches 158; Conservative 64; Mismatches 127; Indels 145; Gaps 10;

QY 2 ADVLISGCTGYVPEDGLTAQQLFASAD-----GLTYNDFLLPGFIDEIADVDLTS 53
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 12 SDLVYS--PYVRMGGLTTPDPTGDDPHKVMAGLTFDDVLLPAASDVPAATDTS 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 54 ALTKRITLTPFLISSPMDTYEADMATAMALMGIGFIHN----- 94
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 QLTNRIRLKLVPSSAMDTVESRMAIAMARAGMGVLRHMLPYAEQAGVEMVKRSEAG 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 95 -----CTPE----- 98
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 129 MYTPDPVTCRPNTLAQDALCARERISGLPVYDDGALVGLITNRDMKFEVDQKQVAEV 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 99 -----FOANEVK-----VKPKDKT----- 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 MTKAPLITAGCGVSASALGLLRNRIKLELPVVDGRGLTGLTYVKDPVKTQHPLATKD 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 114 -----LLCGAVGTREDDKYRLDLTQAGVDYIVLSSGNSVYQIAMVHYIKQY-PLIQ 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 SDGRLVGAAGVGDADVNRMMMLVDAGVDLVDTAHRMLVLDVNGKLKSEVDGVE 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 169 VIGENVVTAQAOKLIDAGVDGLRYMGCGSICITQEVNACGPGQVYVYVAEYARFG 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 309 VVGGNVATRSAAALVADAGAAVKGVPSCITTRVYAGVGAQIQTILAEVAACRAG 368
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 VPITADGGIQTGVHVKVVALGASTVMGSLIAATTEAPGEYFSDGVRLLKRYMGSLD 288
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 369 VPVIADGGIQTSGDIARALAGASTAMLGSLAGTAEPAGELIFVNGKQYKSYRMGSLG 428
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 289 AME-----KSSSSOKRYPSE-----DKYKIAQVSSGSDKSIQKFFVYLLAGIOHGD 340
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 429 AMRGRGATSYSKDRYFADALSDKLT-VPEGIEGRVFRGRLPSSVYIHLQTLGLRAMGY 487
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 341 IGARSLVLRSMY 354
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 488 TGSPTIEVLQAQAF 501
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 22

```

```

IMDH_BORBU
ID IMDH_BORBU STANDARD; PRT; 404 AA.
AC P49058;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GNAB OR BBH17.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Plasmid cp26 (circular 26 kb).
OX Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OY NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi."
RL Nature 390:580-586(1997).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=20222989; PubMed=10758003;
RA McMillan F.M., Cahoon M., White A., Hedstrom L., Petsko G.A.,
RA Ringe D.;
RT "Crystal structure at 2.4-A resolution of Borrelia burgdorferi inosine
RT 5'-monophosphate dehydrogenase: evidence of a substrate-induced
RT hinged-lid motion by loop 6."
RL Biochemistry 39:4533-4542(2000).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
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CC -----
DR EMBL: U13372; AAA53247.1; -.
DR EMBL: AE000792; AAC66314.1; -.
DR PDB: 1EEP; 29-MAR-00.
DR TIGR: BBH17; -.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Plasmid;
KW 3D-structure; Complete proteome.
FT BINDING 229 229 IMP.
SQ SEQUENCE 404 AA; 43767 MW; A91D6D6C5CE522F1 CRC64;

```

```

Query Match Summary          30.7%; Score 601; DB 1; Length 404;
Best Local Similarity       37.1%; Pred. Mol. 4.3e-38;
Matches 149; Conservative   61; Mismatches 134; Indels    58; Gaps      6;

OY 28 DGLTYNDELILPGFIIDFADEVDLTSALTRKLTTLTKPLISSPMDVYTEADMAIAMAIMG 87
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  3 EALFTEDDVSLIRKSSSVLPSEVSATKTOLTKNLSLNIPLSSAMDVTYESQMAIALAKEGG 67
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 88 IGFTHNCTPEEQANDEVRKY--KFDKT----- 113
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  68 IGIIHKMNSIEAQRKEIEVKYFKFOKTIINTNGDTNEOKPEIFETAKQHLEKSDAYKNMEH 127
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 114 -----LLCGAAVGTRBDKRYRLDLOAGADVVLVDSSOGNSYYOIAMVHY 159
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  128 KEDFPNACKDLNNKRIRGVGAANSIDTITERVELYKAHADLVLDVSAHSHSTRITIELLK 187
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 160 IKQKYPHLQVIOTGCVNTVTAQAANKLIDAGVDGELRVGMCGSICITOEVMAAGRPOGTAVYK 219
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  188 IRTKYPNDLIANGNLIVTREKALDILSVAGCDLKVGIGPESICTTTIHVAGVPQTALICD 247
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 220 VAEYARRRGVPIIADGCIOTVGHVVKKALALGASVYMMSGLAATTAPAGEYFFSDGVRLK 279
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  248 VEACNNNTNICIIAGCGRFGSGDVYKAIAGAASVMIGNLFAGTKESPSEETIYNKPKR 307
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 280 KYRGGSIDAMKSSSSSQKRYFS -EGDKY--IAQGVSSIODKSIOKFVYLLAGIOL 336
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  308 SYVGGSSISAMKRGSKS --RYFTLNNEPKKLVPBGIECMWYSCKLMDILLQLKGILMS 365
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 337 GCODIGARSLSYLRSMMYSGELTFEKRMTSAQIEEGVHGILHS 378
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB  366 GMGYLGCAATISDLKI-----NSKPYKISHSLKESHPIHDVFS 402
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 23
IMDH_ECOLI STANDARD: PRF: 488 AA.

AC P06981.P76574; P78202;
AD 01-APR-1968 (Rel. 07, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
GN dehydrogenase) (IMPDH) (IMPD)
GC GUA OR GUAR OR B2508 OR Z3772 OR ECS3370.
OS Escherichia coli, and
OC Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RA MEDLINE=85215547; PubMed=2860637;
RT Tiedeman A.A., Smith J.M.;
RT "Nucleotide sequence of the guaB locus encoding IMP dehydrogenase of
RT Escherichia coli K12."
RL Nucleic Acids Res. 13:1303-1316(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97349980; PubMed=9205637;
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsunashi N.,
RA Mizubuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
```

RA Osilima T., Oyama S., Saito N., Sampel G., Saoh Y., Sivasundaram S.,
RA Tasumi H., Takahashi H., Takada J., Takemoto K., Uehara K., Mada C.,
RA Yamagata S., Tokiuchi T.:
RT "Construction of a contiguous 874-kb sequence of the *Escherichia coli*
RT - K12 genome corresponding to 50,0-68.8 min on the linkage map and
RT analysis of its sequence features".
RL DNA Res. 4:91-113(1997).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / FDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Pena N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postal G., Hackett J., Klink S., Boulton A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimailanta E.T., Potomousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.:
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7".
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258766;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsundo H., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kumata S., Shiba T., Hattori M., Shinagawa H.:
RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
RT O157:H7 and genomic comparison with a laboratory strain K-12".
RL DNA Res. 8:11-22(2001).
RN [6]
RP SEQUENCE OF 1-96 FROM N.A.
RC MEDLINE=86056959; PubMed=2998937;
RA Thomas M.S., Driablie W.T.:
RT "Nucleotide sequence and organisation of the *gua* promoter region of
RT *Escherichia coli*".
RL Gene 36:45-53(1985).
RN [7]
RP SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.:
RT "Comparing the predicted and observed properties of proteins encoded
RL in the genome of *Escherichia coli* K-12".
RN Electrophoresis 18:11259-1313(1997).
RN [8]
RP PARTIAL SEQUENCE OF 1-11.
RC STRAIN=K12 / W3110;
RA Frutiger S., Hughes G.J., Pasquali C., Hochstrasser D.F.:
RL Submitted (FEB-1996) to the SWISS-PROT data bank.
RN [9]
RP SEQUENCE OF 1-5.
RC STRAIN=K12 / W3110;
RX MEDLINE=98291876; PubMed=9629924;
RA Molloy M.P., Herbert B.R., Walsh B.J., Tyler M.I., Traill M.,
RA Sanchez J.-C., Hochstrasser D.F., Williams K.L., Gooley A.A.:
RT "Extraction of membrane proteins by differential solubilization for
RT electrophoresis using two-dimensional gel electrophoresis".
RL Electrophoresis 19:837-844(1998).
RN [10]
RP CATALYTIC ACTIVITY: inosine 5'-phosphate + NAD(+) + H(2)O =
RC xanthosine 5'-phosphate + NADH.
RN [11]
RP PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC [12]
CC SUBUNIT: HOMOTETRAMER.
CC [13]
CC MISCELLANEOUS: IMP DEHYDROGENASE FROM OTHER BACTERIAL SOURCES HAS
CC BEEN SHOWN TO VARY WIDELY WITH RESPECT TO ALLOSTERIC PROPERTIES,
CC SIZE AND SUBUNIT COMPOSITIONS.
CC [14]
CC MISCELLANEOUS: IMP DEHYDROGENASE SUBUNIT OF *E. COLI* CONTAINS A
CC CYSTEINE AT THE IMP BINDING SITE & IS INHIBITED IN A SIMPLE
CC COMPETITIVE MANNER BY GMP. IT DOES NOT EXHIBIT ALLOSTERIC
CC PROPERTIES AS DOES IMP DEHYDROGENASE FROM *BACILLUS SUBTILIS* OR
CC *SALMONELLA TYPHIMORIUM*.
CC [15]
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.

CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 DR EMBL: X02209; CAA26133.1; ALT_INIT.
 DR EMBL: AE000337; AAC75561.1; -.
 DR EMBL: D90880; BAA16395.1; ALT_INIT.
 DR EMBL: AE005480; AAC57619.1; -.
 DR EMBL: AP002561; BAB36793.1; -.
 DR EMBL: M10101; AAB18618.1; -.
 DR PTR: A23023; DECIPT.
 DR HSP: PA9058; IEEP.
 DR SWISS-2DPAGE: P06981; COLI.
 DR EcoGene: EG10421; quab.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
 DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
 KW CBS domain; Complete proteome.
 FT DOMAIN 90 143 CBS 1.
 FT BINDING 151 206 CBS 2.
 FT CONFLICT 206 206 IMP (POTENTIAL).
 FT SEQUENCE 488 AA; 52022 MW; B0FDDA786779C98E CRC64;
 SQ
 Query Match 30.7%; Score 600.5; DB 1; Length 488;
 Best Local Similarity 32.9%; Pred. No. 5.8e-38;
 Matches 149; Conservative 59; Mismatches 112; Indels 133; Gaps 7;
 Oy 28 DGLTYNDPLIPGFTIDPIADEVDLTSAITRKITLTKPLLISSPMDTVTEADMAIMALMG 87
 Db 7 EALTFDVLVPAHSTVLPNTADLTQITKTRINIPWLSAMPTVTEARALALAOGG 66
 Oy 88 IGFTHNCTPEFOANEVRYKK----- 109
 Db 67 IGFTHKMSITROAEVRAKAKHESGVYTPQIVLPPTTLREVKELTERNGFAGIPVTE 126
 Oy 110 ----- 109
 Db 127 ENELVGIITGRDVFVTDLNPVSVMTPKRLVTVREGAREVVLAKMHEKREKALV 186
 Oy 110 -----FDKT-----LLCGAAGTREDKRYLDLLTQAGDVIV 142
 Db 187 DDEPHLIGMITVKDFQKERRKNACKDEQGLRYGAAGAAAGNEERDALVAAGVDLL 246
 Oy 143 LDSSGNSGVYQIAWVHYIKQYRPHLOVIGNVVTAQAOKNLLIDAGVDSLIRMGSGSICI 202
 Db 247 IDSSHGSEGVQIRRETRAKYPDQITIGNVVTAAGARALAEAGCSAVKGIIGSGICT 306
 Oy 203 TOEVMACRPGGTAVYKVAEYARFGVPIIDAGIQIVGHVVKALALAGSTVMMGSLAA 262
 Db 307 TRITGVGVPIITAVADVALEGGIGIPVADGGIRFSGDLAKAIAAGASAVMVGSLAG 366
 Oy 263 TTEAPGEYFSDGVRLKKYRGMGLDAMEKSSSOKRYF---SEGDKYIAQVSGSIQD 319
 Db 367 TEESPGTELELYGGRSYKSRGMGLSAGMSKSSD--RYFGSDNADKL-VPEGIGRVAY 423
 Oy 320 KGSIQKFPYVLIAGIQCQDI-GARSLVARS 351
 Db 424 KGRLEIHHQMGGLR-SCMGLTGCGLTDELRT 455

RESULT 24
 ID IMDH_MYCLE STANDARD; PRT; 529 AA.
 AC 049729;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Icosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
 DE dehydrogenase) (IMPDH) (IMPD).
 GN GAB OR ML0387 OR B1620_C3_238.
 OS Mycobacterium lepreae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterinae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxId=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith D.R., Robison K.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeller K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Felwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus";
 RL Nature 409:1007-1011(2001).
 CC -1- CATALYTIC ACTIVITY: Icosine 5'-phosphate + H₂O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIOE TO GMP BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 DR EMBL: U00015; AAC43232.1; -.
 DR EMBL: AL583918; CAC29895.1; -.
 DR HSP: P12268; LB30.
 DR Leptoma; ML0387; -.
 DR InterPro: IPR000644; CBS.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00571; CBS; 2.
 DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 DR SMART: SM00116; CBS; 2.
 DR PROSITE: PS00487; IMP_DH_GMP_RED; FALSE_NEG.
 DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
 KW CBS domain; Complete proteome.
 FT BINDING 341 341 IMP (POTENTIAL).
 FT SEQUENCE 529 AA; 54814 MW; 1565C62EC9529870 CRC64;
 SQ
 Query Match 30.7%; Score 600.5; DB 1; Length 529;
 Best Local Similarity 31.6%; Pred. No. 6.4e-38;
 Matches 156; Conservative 64; Mismatches 129; Indels 145; Gaps 10;
 Oy 2 ADYLISGCTGVPEGLTAQOLFASAD-----GLTYNDPLIPGFTIDPIADEVDLT 53

```

Db      12 SDFVA---SYRRLGGIMDDPAATGGDNPHKVAMLGTFEDVLLPAAASVVPATADISS 68
OY      54 ALFRKTLKPLTSPMDVTEADMAIAMLGIGIFHN-----94
Db      69 QLFKRIKRLKPLVSSAMDYTEARMAIAMAARAGMGVLRNLPVGEQAGOVETVKSEAG 128
OY      95 -----CPE-----98
Db      129 IMVDPYTCRPDNTLAQVGLCARFISGLPVVDSGALAGIITNRDMRFEVDGSKOAEV 188
OY      99 -----FANEVYK-----YKFKDT-----113
Db      189 MKRTPLTAAEGVSADALGLLRNKIEKLPVVDGGRLTGLITVDFVTECHPLATKD 248
OY      114 -----LLCGAAGVTRDDKYRLDLTQAGVDVITLSSQGSVYQIOMVHNHIXKY-Phlo 168
Db      249 NGRLLVGAAGVGVGDAWVRAMMLVDAAGVDVITVTAHNRLLVLMVGKLVKEIGDRVQ 308
OY      169 VIGGNVNTAAQAKNLIDAGVDGLRVGSGSICITQEVMAAGRPCTAYVVAEYARRFQ 228
Db      309 VIGGNVNTSAAALVAGADAVKGVGSGSTCTTRVAVGAPQITALEAVALAGSPAG 368
OY      229 VPIAAGGIGTGVHVYKALALGASTVMGSLAATTEAPGEYFSSGVRLKTRGMSLD 288
Db      369 VPIADGGIGTQSGDIKALAAAGSTMLSLAGTAEAPELLFVNGKOFKSYRGMSLD 428
OY      289 AME-----KSSSQKRFSEK-----DKVTAQVSGSIOGKQKFPVYLIAGIOGCD 340
Db      429 AMOGRGDKSYKDRYFADALSEDKL-VPEGIEGRVPRPGLSVITHOLVGLRAMGY 487
OY      341 IGARSLSVLRSMY 354
Db      488 TGSPTIEVLQQAQF 501

RESULT 25
IMDH_PASMO STANDARD; PRT; 487 AA.
AC Q9LB7;
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE 16-OCT-2001 (rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
GN GUAB OR PM0295.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RA Fuller T.E., Kennedy M.J., Lowery D.E.;
RT "Identification of Pasteurella multocida virulence genes in a
RL septicemic mouse model using signature-tagged mutagenesis.";
RN Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
RP [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.U., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER EOKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF237921; AAF68407.1; -.
DR EMBL; AE006064; AAK02379.1; -.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT DOMAIN 91 144 CBS 1.
FT DOMAIN 153 206 CBS 2.
FT BINDING 305 305 IMP (POTENTIAL).
SQ SEQUENCE 487 AA; 52007 MW; 0871DB0893B8FCA CRC64;

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Query Match 30.1%; Score 587.5; DB 1; Length 487;
Best local similarity 32.5%; Pred. No. 5,5e-37;
Matches 147; Conservative 59; Mismatches 114; Indels 133; Gaps 7;

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OY 28 DGLTVDFILNGFIDFINDVDLTSLRKTITKPLTSPMDVTEADMAIAMLG 87
Db 7 EALTEDVLLVPAHSTVLNPTADLSTQTLTKTLNIPMLAAMDVTEYKLAISLQEGC 66
OY 88 IGFHNCTPEFOANEVRKKFED-----111
Db 67 IGFHNKMSIERQAEVRKVKKEGSIQSDPYVSPTLSLAEISELYKKNFASPPVVD 126
OY 112 -----KT-----113
Db 127 EKNLVGIITGRDTRFVTDLNKTVADEPMPKARLVYVRNASHDELFGMLHTRHEKVLV 186
OY 114 -----LLCGAAGVTRDDKYRLDLTQAGVDVITV 142
Db 187 SDDFKLKGMITLKDVKOSEOKPOACKDEGRRLRVGAAGVAGGNERIDALYKAGVDVLL 246
OY 143 LPSQGSVYQIAMVHYIKQYPHLOVIGNNVTTAAQAKNLIDAGVDGLRVGSGSICI 202
Db 247 IDSNGHSGEGLQVRVETRAKYPDLPIVAGNVATAGALALADAGSAVKVIGPGSICT 306
OY 203 TOEVMACGRPGCTAYVKAIEYARRGVPIIADGGIOTGVHVYKALALGASTVMGSLAA 262
Db 307 TRIVTGVGPQITAIADAAEALKRGIPIVIADGIRFSGDISKALAAAGSCVMVGSMPFAG 366
OY 263 TTEAPGEYFSSGVRLKVRGMSLDAEMKSSSQKRYF---SEGGKYVIAAGVSSIDD 319
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Db 424 KGFKEIITHQNGGLR-SCMGLTGCAITDELRT 455

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Search completed: September 26, 2002, 08:28:34
Job time: 138 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2002, 08:24:46 : Search time 32.36 Seconds

(without alignments)
1318.057 Million cell updates/sec

Title: US-09-853-918-30

Perfect score: 1955

Sequence: 1 MADYLLSGTGYVEDGLTA.....MSAQIEGCVHGLHSYKRLY 384

Scoring table:

BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

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- 22: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1778.5	91.0	604	22	ABG22269	Novel human diapo
2	1655	84.7	514	11	AAK05431	Chinese hamster IM
3	1653	84.6	514	11	AAK05432	Human IMPDH. Hom
4	1557	79.6	430	22	ABG23731	Novel human diapo
5	1348.5	69.0	537	22	ABB58547	Drosophila melanog
6	1348.5	69.0	537	22	ABB58547	Drosophila melanog
7	1016	52.0	502	21	AAK30888	Arabidopsis thalia
8	1013.5	51.8	503	21	AAK20989	Arabidopsis thalia
9	1007.5	51.5	503	21	AAK43108	Arabidopsis thalia
10	986.5	50.5	371	20	AAV08965	A. gossypii inosin
11	963	49.3	287	22	ABG07490	Novel human diapo

12	886	45.3	443	21	AAK30889	Arabidopsis thalia
13	878.5	44.9	444	21	AAK20990	Arabidopsis thalia
14	872.5	44.6	444	21	AAK43109	Arabidopsis thalia
15	860	44.0	435	21	AAK30890	Arabidopsis thalia
16	852.5	43.6	436	21	AAK20991	Arabidopsis thalia
17	846.5	43.3	436	21	AAK43110	Arabidopsis thalia
18	691.5	35.4	403	22	AAK70679	S cerevisiae apopt
19	677.5	34.7	215	22	ABG22268	Novel human diapo
20	632	32.3	489	22	AAK36360	Pseudomonas aerugi
21	625	32.0	185	21	AAK58731	Breast and ovarian
22	616	31.5	488	22	AAK2607	S. epidermidis ope
23	615	31.5	506	22	AAK90418	C glutamicum prote
24	615	31.5	506	22	AAK80106	Corynebacterium gl
25	605.5	31.0	489	21	AAV97820	Pseudomonas sp. WF
26	600.5	30.7	488	22	AAU29344	Novel mar regulate
27	587.5	30.1	487	21	AAK4532	Virulence gene pro
28	586.5	30.0	492	22	AAK03593	Haemophilus influe
29	574.5	29.4	488	22	AAK01060	CPE 63 protein seq
30	574	29.4	481	19	AAW98634	H. pylori GHPD 307
31	572	29.3	481	19	AAV11109	H. pylori ORF hp8e
32	528.5	27.0	514	22	AAU58049	Propionibacterium
33	516	26.4	152	21	AAK27200	zee mays protein f
34	502	25.7	161	21	AAK03970	Human secreted pro
35	491	25.1	485	21	AAK96466	Putative P. abyssi
36	484	24.8	140	21	AAK27201	zee mays protein f
37	470	24.0	133	20	AAK27202	zee mays protein f
38	447	22.9	266	21	AAV34772	Chlamydia pneumoni
39	376	19.2	95	22	AAO04552	Human polypeptide
40	362.5	18.5	479	22	AAU04859	Microthospora eve
41	351.5	18.0	477	22	AAK92691	C glutamicum prote
42	351.5	18.0	477	22	AAK80109	Corynebacterium gl
43	351	18.0	155	22	ABG22266	Novel human diapo
44	351	18.0	217	21	AAK58491	Lung cancer associ
45	345	17.6	348	19	AAW52169	Human MKK3-interac
46	345	17.6	348	22	AAK38661	Human polypeptide
47	345	17.6	348	22	AAK66724	Human dehydrogenas
48	345	17.6	366	19	AAW37945	Amino acid sequenc
49	341	17.4	66	22	ABG22265	Novel human diapo
50	341	17.4	325	22	AAU352185	Enterococcus faeca
51	341	17.4	325	22	AAU33399	Enterococcus faeca
52	339	17.3	325	22	AAU35850	Helicobacter pylor
53	333.5	17.1	151	20	AAV08964	A. gossypii inosin
54	331.5	17.0	328	22	AAU37668	Streptococcus pneu
55	331.5	17.0	447	22	AAK40447	Human polypeptide
56	327.5	16.8	447	22	AAK40448	Human polypeptide
57	326.5	16.7	409	22	AAK38662	Human polypeptide
58	317	16.2	347	22	AAU34442	E. coli cellular p
59	312	16.0	325	22	AAK83101	S. epidermidis ope
60	307	15.7	350	21	AAV93154	Human guanosine mo
61	295	15.1	325	22	AAU37145	Staphylococcus aur
62	295	15.1	325	22	AAU37462	Staphylococcus aur
63	295	15.1	347	22	AAU38321	Salmonella typhi c
64	290	14.8	156	22	ABG22267	Novel human diapo
65	289.5	14.8	471	22	AAU45471	Propionibacterium
66	282	14.4	55	22	AAK75199	Human colon cancer
67	263	13.5	220	22	ABG07806	Novel human diapo
68	260	13.3	178	22	AAK80108	Corynebacterium gl
69	256.5	13.1	732	22	ABG30033	Novel human diapo
70	215	11.0	174	22	AAK82435	S. epidermidis ope
71	209.5	10.7	359	22	ABG07805	Novel human diapo
72	208	10.6	158	22	AAK80107	Corynebacterium gl
73	192.5	9.7	378	22	AAU58050	Propionibacterium
74	190.5	9.7	265	21	AAK58994	Human prostate can
75	190.5	9.7	292	22	AAU23259	Novel human enzyme
76	190.5	9.7	292	22	AAK43631	Human polypeptide
77	190.5	9.7	292	22	AAU21663	Novel human neopla
78	179	9.2	87	20	AAV35743	Chlamydia pneumoni
79	161	8.2	374	22	AAK90420	C glutamicum prote
80	161	8.2	374	22	AAK80117	Corynebacterium gl
81	131	6.7	401	22	AAK38235	Salmonella typhi c
82	127	6.5	324	22	AAK02209	Streptococcus pneu
83	126	6.4	79	21	AAK02568	Human secreted pro
84	125	6.4	324	22	AAK01010	CPE 9 protein sequ

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85 124 6.3 324 22 AAU37766 Streptococcus pneu
86 117 6.0 318 22 AAU53326 Enterococcus faeca
87 116.5 6.0 255 21 AAG27445 Arabidopsis thalia
88 116.5 6.0 255 21 AAG27444 Arabidopsis thalia
89 116.5 6.0 260 21 AAG27443 Arabidopsis thalia
90 116.5 6.0 312 21 AAG37849 Arabidopsis thalia
91 116.5 6.0 317 21 AAG36985 Arabidopsis thalia
92 116.5 6.0 317 21 AAG53311 Arabidopsis thalia
93 116.5 6.0 338 21 AAG27848 Arabidopsis thalia
94 116.5 6.0 343 21 AAG36984 Arabidopsis thalia
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96 116.5 6.0 358 21 AAG37847 Arabidopsis thalia
97 116.5 6.0 363 21 AAG36983 Arabidopsis thalia
98 116.5 6.0 363 21 AAG53309 Arabidopsis thalia
99 115 5.9 351 22 AAU36391 Pseudomonas aerugi
100 114.5 5.9 333 21 AAG55063 Arabidopsis thalia
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ALIGNMENTS

RESULT 1

ABG22269 standard; protein: 604 AA.

ABG22269; 18-FEB-2002 (first entry)

Novel human diagnostic protein #22260.

Human: chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

NC200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001MO-US08631.

31-MAR-2000; 2000US-0540217.

23-AUG-2000; 2000US-0649167.

(HYSE-) HYSEQ INC.

Dymanac RT, Liu C, Tang YT;

WPI: 2001-639362/73.

N-PSDB; AAS86456.

New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

Claim 20: SEQ ID NO 52628; 103bp; English.

The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations in

CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pcl_sequences](http://wipo.int/pub/published_pcl_sequences).

XX Sequence 604 AA;

Query Match 91.0%; Score 1778.5; DB 22; Length 604;

Best Local Similarity 71.3%; Pred. No. 1,3e-165; Mismatches 12; Indels 131; Gaps 2;

Matches 367; Conservative 5; Mismatches 12; Indels 131; Gaps 2;

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DB 90 madylisgvgypedgltaqqlfasaddltyndfllpgdfididevdltsaltrkit 149

QY 61 LKTPPLISSPMDTYTEADMAIAMLGIGFIHNCPTPEFQANEVRYKVKFKDK----- 112
DB 150 lktpplisspmdtyteadmalamalgigfihncptpefanevrkvnklegfildpv 209

QY 113 ----- 112
DB 210 lpshtvgdvlegkmrhgfsqipitetgmsklvgivtsrdidflaekdhtllsevm 269

QY 113 ----- 112
DB 270 prlelvapagvclkeanellgrskkklplvndcdelvaliartdlkserdylaskds 329

QY 113 - - - - - 170
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QY 171 GGNVYTAQAOKNLIDACVDDGLRVGMGSGSICITQEWMAAGRPQGT -AVYVAEYARREGV 229
DB 390 ggnvtaaqaknllidagvdlrvmgsgsictqevnacgrrpqgtccvtxaeayarfgy 449

QY 230 PIADGCIQTVGHVVKALAGASTVMKGSLLAATTEAPGEFTSDGYRLKRYKMGSLDA 289
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QY 290 MEKSSSSQKRRFSEGDYKKAQGVSGSIDKGSIOKRVPLIAGIOHCODIGARSLVL 349
DB 510 meksssqkrrfsegdvkvkaqgvsgsidkgsioqrvtplliagiqhgcddigarslsvl 569

QY 350 RSMWYSGELKFEKRTMSAOIEGGVHGHSYEKRLY 384
DB 570 rsmwysgelkfekrtsapqieggvnhginsyekrily 604

RESULT 2

AA05431 standard; protein: 514 AA.

AA05431;

31-AUG-1990 (first entry)

Chinese hamster IMPDH.

Inosine 5'-mono-phosphate dehydrogenase; hepatomas;

guanosine monophosphate.

Cricetulus sp.

WO9001545-A.

22-FEB-1990.

02-AUG-1989; 89WO-0000344.

XX	DT	17-OCT-2000	(first entry)
XX	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 37006.	
XX	XX	Protein identification: signal transduction pathway; metabolic pathway; hydridisation assay; genetic mapping; gene expression control; promoter termination sequence.	
XX	OS	Arabidopsis thaliana.	
XX	XX	EP1033405-A2.	
XX	PD	06-SEP-2000.	
XX	PF	25-FEB-2000; 2000EP-0301439.	
XX	PR	25-FEB-1999; 99US-0121825.	
XX	PR	05-MAR-1999; 99US-0123160.	
XX	PR	09-MAR-1999; 99US-0123548.	
XX	PR	23-MAR-1999; 99US-0125788.	
XX	PR	25-MAR-1999; 99US-0126264.	
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XX	PR	01-APR-1999; 99US-0127462.	
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XX	PR	18-JUN-1999; 99US-0139461.	
XX	PR	18-JUN-1999; 99US-0139462.	
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QY	75	EADMAIAALWIGGIGFHHNCPREOANRVRKFF-----	110	
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QY	111	-----	110	
Db	125	psfsvfsqgtllrpkllgysksewsmskddqevklydymscenkdyypwddldlk	184	
QY	111	-----DKTLGCAAVGTRE	124	
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PR 28-OCT-1999; 99US-0161920.


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XX AAY08965;
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XX 19-AUG-1999 (first entry)
XX
XX A. gossypii inosine-monophosphate dehydrogenase protein fragment 2.
XX
XX Purine biosynthesis; phosphoribosylpyrophosphate synthetase; KPR1; KPR2;
XX glutamine-phosphoribosylpyrophosphate amidotransferase; ADE4; GUA1;
XX IMP-dehydrogenase; GUA1; GMP-synthetase; GUA2; PRPP synthetase; mouth;
XX riboflavin; vitamin B2; treatment; inflammation; throat; mucosal layer;
XX skin disorder.
XX
XX Ashbya gossypii.
XX
XX EP927761-A2.
XX
XX 07-JUL-1999.
XX
XX 08-DEC-1998; 98EP-0123331.
XX
XX 23-DEC-1997; 97DE-1057755.
XX
XX (BADI ) BASF AG.
XX
XX Hoeffen HM, Jimenez A, Pompejus M, Revuelta Deval JL;
XX Santos Garcia MA, Seuberger H;
XX
XX WPI, 1999-373465/32.
XX
XX N-PSDB; AAX78081.
XX
XX Ashbya gossypii purine biosynthesis enzymes and related genes for
XX production of riboflavin
XX
XX Claim 13; Page 33-34; 48pp; German.
XX
XX This invention describes novel enzymes involved in purine biosynthesis
XX in Ashbya gossypii. The enzymes described in the invention include
XX Phosphoribosylpyrophosphate (PPRP) synthetases KPR1 and KPR2
XX glutamine-phosphoribosylpyrophosphate amidotransferase (ADE4)
XX IMP-dehydrogenase (GUA1) and a GMP-synthetase (GUA2). The nucleic acid
XX sequences encoding the enzymes involved in purine biosynthesis are used
XX to genetically modify microorganisms, for the production of riboflavin.
XX Riboflavin, also known as vitamin B2, is essential in humans and animals
XX and is used to treat inflammation of the mouth and throat mucosal layer
XX as well as inflammation in skin disorders. This sequence represents a
XX fragment of the inosine-monophosphate dehydrogenase protein encoded by
XX the GUA1 gene represented in AAX78081.
XX
XX Sequence 371 AA;
XX
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Best Local Similarity 56.9%; Pred. No. 3.9e-88;
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DB 62 lvdgeglvsmstrcdlknkngysplaskadt----- 93
OY 101 ANEVRKRVKFDKTLTGAAVGTREDKRYRLDLLTGADVIVLDSQNSGYOIAMVHYI 160
DB 94 -----kqlcggaigtldedrqqlamlveagldvvlldssgnsqvdimikvl 142
OY 161 KOKYRHLQVIGSNVYTAQAKMLIDAGVDGLRVGKCGSICITOEYMACGRQGTAVYKV 220
DB 143 ketfpdlqylagvntvteqaaasllhagadgllrgmgsstictgvmagcgrpgtavyv 202
OY 221 AEYARFGVPIITADGIGTGVHVAALAGASTVMMGSLAATTAFTAPGFEFSDGVRLKK 280
DB 203 tgfahqfyvpciadgvgvqnlghltkatalagastvmmgmlagctvpgaylfrdgrrlkt 262
OY 281 YRGMGSLDAMEKS---SSSOKRYFSEGDVKVRIAQVSGSIODKSGIOKVFVYLLAGIOH 336

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DB 263 yrgmgsldamqktvkvgaatsaryfsesdkvlgagvgvsvldkgsikkylpylgnlqh 322
OY 337 GCODIGARSLSVLRSMYSGELKFEKRIMSQAIEGVGIGHSYERLY 384
DB 323 scqdlgvrslvlfrekvdsvsvftrcpsaqleggvmlhsyekrlf 370
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XX 13-FEB-2002 (first entry)
XX
XX DE Novel human diagnostic protein #7481.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
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XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS71677.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 37849; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
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XX Sequence 287 AA;
XX
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Query Match 49.3%; Score 963; DB 22; Length 287;
Best Local Similarity 68.9%; Pred. No. 5.4e-86;

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Db 61 LKTPLISSPMDTVTEADMAIMALMGIGFTIHNCPTPEFOANEYKVKKED----- 111
61 lktpliisspdtl---adialamalmgigfihncptefgkvekvkfkfegfildpvt 117

QY 112 -----KTLGSAVGTRE 124
118 ltpstvgdvleakmrhngfsqiptletctlgsklnrdyplasskshkqllrqaavtpe 177

QY 125 DDKYRLDLTQAGVDVITVLDSSQGSNSVYQIAMVHYIKQYEPHLQVIGSNVTAAQAKNLI 184
178 ddkyrldlftcgaydvvnlldisgnsyqlatvhyikqyphldvlg---mtaegaknll 234

QY 185 DAGVDGLRVGMGCGSICITQEVMAACGRPGCTAVYKVAEYARRECVPIIADGCI 237
235 daavdgltlrimgcgslctqevmaccgpgpqlalykvaeyalcfgvsladgyl 287

RESULT 12

AAG30889
ID AAG30889 standard; Protein: 443 AA.

AC AAG30889;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 37007.

KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123548.
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Best Local Similarity 42.0%; Pred. No. 3.7e-78;
Matches 187; Conservative 47; Mismatches 79; Indels 133; Gaps 2;
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QY 111 ----- 110
Db 61 vddfgpsfivfsqtlgllgvyksesmsmkddqkevkiydmkscenkdyvypwd 120
QY 111 -----DKTLGCAA 119
Db 121 idldkleavledkqgfvvlekegetvnyvtdkddvervqyphlgsgvtgadmkmvgaa 180
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QY 240 VGHVVKALAGASTVMMSGLAATTEAPGEPFSDGVRFLKKRYMGSLDAMEKSSSOKR 299
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QY 300 YFSEGDVKRIAGVSGSIODKGSIQKFPVYLLAGIOHCCODIGARLSVLRSMYSGELK 359
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AC AAG20990;
XX
DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 23384.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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Query Match	44.68;	Score 872.5;	DB: 21;	Length 444;
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Gy	101	-----ANEVRKVKKFKDXT-----LLCGA	118
Db	121	eidfeklefledkqkgfvnlardgetynvvltkdldlqrkvkypkspgtvgppdgemmva	180
Gy	119	AVGTREDDKRYRLDLLOAGADVVLDDSSGNSGVNIOAWHVIKKQYRPHLOWIGANNVTAA	178
Db	181	aigrtesdkerlehlrvnvgnavvildssgnsiygltemlkkyvkttypedelcignvntmy	240
Gy	179	QAUKLIDAGVDGLRVMGCGSICITOEVMACGRPOGTAIVYVAETARRRFGVPPIADSGIO	238
Db	241	qaquillagaydqjlrvmgsqslctbevcavargatavrvfvcslaagsqlpvadlsgs	300

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Query Match              44.6%; Score 872.5; DB 21; Length 444;
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DB      1 mdvtvshmaamaslgygiyvhmglaagaslrqakslkphlaadagkyfpeyeits
OY      101 -----
DB      61 ldfafpsfvfveqgtmttprkllygvtksgykrmyneqremkilydymkscdsadycvpw
OY      101 -----
DB      121 eidfeklefyedkxgkfjvnlrdergetynvltkdldiqvkaypkspgvtvgpdgemwva
OY      101 -----ANFVRKVKFKDPT-----LLCGA 118
DB      121 eidfeklefyedkxgkfjvnlrdergetynvltkdldiqvkaypkspgvtvgpdgemwva 180

119 AVGREDDDKRLDLTLAQAGDVIVLSDSGANSVYOIAWAVHIKKRYPHLOWIGGNVTAA 178
+:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      181 aigrdeskerlllvnygvnavvlidssagnsygltemlkyyvkttyelwdlggnvvltmy 240
+:::|||||DGVDGIRVMGGCSICITIOEWMACGRPOGTAVTVVAETARRRFVPITADSGIO 238
+:::|||||DGVDGIRVMGGCSICITIOEWMACGRPOGTAVTVVAETARRRFVPITADSGIO 238
DB      241 gaqqlldagvdgrlvmgsngsictqevcaavrgatavrvfcsciaaqspjrvladgis 300

```


PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
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PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 18-JUN-1999; 99US-0139461.
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PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141844.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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PR 19-JUL-1999; 99US-0144325.
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PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147192.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159294.
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PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.

PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161350.
PR	26-OCT-1999;	99US-0161369.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match 43.6% Score 852.5; DB 21; Length 436;
Best Local Similarity 41.8%; Pred. No. 6.9e-75;
Matches 183; Conservative 45; Mismatches 77; Indels 133; Gaps 4;

OY	78 MAIAALMAGIGIFIHNC-----IPEFANEV-----	104
Dd	1 maaamaslglgvlvhnclaaqasllrqaklkhpriasadavklrpeylatsvdafgrps	60
OY	105 -----RKVKKFDKLTC-----	116
Dd	61 fvfveqtgmtpkrllyvtksqwkrmtyeqemkiydmkscdsdyevrpwdfidekie	120
OY	117 -----GAVGTRDD	126
Dd	121 flvedkqkfvlvrldgelevnvtkdldlrkvkypskspgtlvrgpdgemnvgaalgtresd	180
OY	127 KRLRLDLQAGADVIVLDSOGNSVYQLAMVHYIKOKYRPHLOVIGGNVTAAQAKMLDA	186
Dd	161 kerlehlhnaagvaavvlldssgnsllyqllemikvvkkcybelovlganvemyqaqnllgy	240
OY	187 GVDGLRVNGCCSICITDEVMACGRPOGTAVVVKAETARFRGVPIADGIIQTGVHVVVA	246
Dd	241 gvdglrvngsgslctltgevcavgqrgetavykvccslaarsgilpyladgglsnshlvka	300
OY	247 LALGSTVMMSGLLAATPARGEFFPSDCVRLKTKRGMSLDAMESSSOXRYESEGCX	306
Dd	301 lvgaslvmmsgflagstearpgyeftngkrlikkyrgmgsleamtk--gsddrylgdklk	358
OY	307 VKIAGVSGSIDDKCSIOKEFYPLLAIIDHGCDIGARLSVLRSMMYGELTFEKRFTMS	366
Dd	359 lkiaagvgavgadcvsvklkplytmhavqvqgdldlgasslgahnlirsnlrlteartga	418
OY	367 AOIEGGVGHLSYEKKRLV	384
Dd	419 agvegvgnglvseyeksf	436

RESULT 17
AAG43110
ID AAG43110 standard; Protein: 436 AA.
XX AAG43110;
XX
DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 53844.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX

	Matches	142:	Conservative	6:	Mismatches	11:	Indels	59:	Gaps	2:
QY	76	ADMAIAMAALMGIGIFIHNNCTPEFGANEVRYKKVED-----								111
Dd	1	adialatalamgmigigifihnnctpefgakevrykkfegfidtpvnltpshtvgdvleakm								60
QY	112	-----KTLICGAAGCTREDDKTRDLULLTOAGVD								139
Dd	61	rhtgfsgiditecvtlgsxlknrdyplaaskdsbhqllrgaaavgtpeddkyrldilltqaayvd								120
QY	140	VIVLDSSGNSGYVOIAMVHYIKORPHILOVIGANGVTAAQAANLIDAGVDGLRVGMCGS								199
Dd	121	vvidlsdgnsyygdiatrchylkqkphhlgvy---mtaaqanlldaaavdlrtigmccgs								177
QY	200	ICTIOEVMACGRPOGTAVYKYAEVARRRGPVIADGGI								237
Dd	178	ictltgevmacggppgtaltalkvaeyslclcfvsiltadgsl								215
RESULT	20									
AU036360	ID	AAU36360 standard; Protein: 489 AA.								
XX	AC	AAU36360;								
XX	DT	14-FEB-2002 (first entry)								
XX	DE	Pseudomonas aeruginosa cellular proliferation protein #350.								
XX	KW	Antisense: prokaryotic cellular proliferation protein; antibiotic: antibacterial; drug design.								
XX	OS	Pseudomonas aeruginosa.								
PN	XX	MOZ00170955-A2.								
PD	XX	27-SEP-2001.								
PF	XX	21-MAR-2001; 2001WO-US09180.								
PR	XX	21-MAR-2000; 2000US-191078P.								
PR	XX	23-MAY-2000; 2000US-206848P.								
PR	XX	26-MAY-2000; 2000US-207272P.								
PR	XX	23-OCT-2000; 2000US-242578P.								
PR	XX	27-NOV-2000; 2000US-253625P.								
PR	XX	22-DEC-2000; 2000US-257931P.								
PA	XX	16-FEB-2001; 2001US-269308P.								
PI	XX	(ELIT-) ELITRA PHARM INC.								
PI	XX	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;								
PI	XX	Yamamoto RT, Xu HH;								
DR	XX	WPJ: 2001-6111495/70.								
DR	XX	N-PSTDB; AAS54219.								
PT	XX	New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids -								
PS	XX	Example 3; Seq ID No 11953; 511pp; English.								
XX	XX	The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are <i>Escherichia coli</i> , <i>Staphylococcus aureus</i> , <i>Salmonella typhi</i> , <i>Klebsiella pneumoniae</i> , <i>Pseudomonas aeruginosa</i> and <i>Enterococcus faecalis</i> . The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen								

CC	for homologous nucleic acids which are required for cell proliferation in
CC	a wide variety of organisms. The present sequence represents an
CC	essential prokaryotic cellular proliferation protein.
CC	Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic
CC	format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
XX	Sequence 489 AA:
XX	
XX	Query Match 32.3%; Score 632; DB 22; Length 489:
XX	Best Local Similarity 33.4%; Pred. No. 3,6e-53;
XX	Matches 159; Conservative 55; Mismatches 130; Indels 132; Gaps 4
OY	26 SADIATYNDLELLPGFIDFIADVDLTSLATRTLTKEPLISSPMDYTEADMAITAMLM 85
DB	5 sgealttdvdllypysevlpkdvskltltltgietlnplvsaaandvttearlaiamag 64
OY	86 GGIGFIHHNCTPEFOANEVRKVKFPD----- 111
DB	65 ggigilnhkmngieqgaeevrkvkhhetaivrdvvtvtpstkliellgmareygsfgfrpv 124
OY	112 ----- 111
DB	125 eggelvgivtgrdlrvkknagdtvaaimprkdklytaregrpleemkaklyenrlekmly 184
OY	112 -----KT-----LLCGAAGTREDDEKVRDLDTTGAVDVI 141
DB	185 vdenfytirgtvftfdlaktvrylaakdegrilrygaavgtgradtgeretvaalvaagvdyv 244
OY	142 VLDSSQGNVQYIAMVHYIKQKYPHLQVIGNVYTAQAOKNLIDAGVDGLRYVMCGGSIC 201
DB	245 vvdtehshskvgyetvrvwtkftprdyvggnataeakaiaaeagadvakvgyisgc 304
OY	202 ITQEVMAAGRPQGAIVYKVAEYARRRCVPIADCGIQTIVGHVKKALAGASTVMMSGLA 261
DB	305 ttrivagvyvpyqisaiaanaalegtvrypladaggyttrfsgdlakamvgaeyvmmgsmfa 364
OY	262 ATTEAPGGEFFPSDSDVRLLKRYKRGMSGLDAMEKSSSSQKRF---SEGDKVKIKQGVSGSIQ 318
DB	365 gteepgeielftgrysksyrgmgsligamsgsgssdrtfydgaasagaeklypegielgryv 424
OY	319 DKGSITQKFPYPLIAGIQHGCODIGARSLSVLRSMYSGELKFEKRTMSAQIEGGVH 374
DB	425 ykgalsaisvhlmgglraamgytgsadiqgmrt-----qpqfvtriltgagmaeshvh 475
XX	
XX	RESULT 21
XX	ID AAB58731
XX	AAB58731 standard; Protein; 185 AA.
XX	AAB58731:
XX	
XX	27-MAR-2001 (first entry)
XX	
XX	Breast and ovarian cancer associated antigen protein sequence SEQ ID 439.
XX	
XX	Human; breast cancer; ovarian cancer; cytosstatic; immunosuppressive;
XX	neurotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
XX	antidiabetic; antiinflammatory; antidiacer; vulnerary; anticonvulsant;
XX	antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
XX	Addison's disease; allergy; autoimmune hemolytic anemia;
XX	autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
XX	multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
XX	cardiovascular disorder; wound healing; neurological disease.
XX	
XX	Homo sapiens.
XX	
XX	WO20005173-A1.
XX	
XX	21-SEP-2000.

Db 369 teesppatevfqgrgkyvrgmstlgamekgsnd--ryfge-dkprkfvpeglegrtay 425
 OY 320 KSSIOKFVYLLAGIOHCCODIGARSLVLRSMVSGELKFEKFRMTSAQIEGSHL 376
 Db 426 kspigdtlylmgvragmytgsenlkkhre-----eaqftrmgpaiaeshphnv 477

RESULT 23

AAG90418
 ID AAG90418 standard; Protein; 506 AA.

AC AAG90418;

DT 26-SEP-2001 (first entry)

DE C glutamicum protein fragment SEQ ID NO: 4172.

KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;

KM organic acid synthesis.

OS Corynebacterium glutamicum.

PN EP1108790-A2.

PD 20-JUN-2001.

PF 18-DEC-2000; 2000EP-0127688.

PR 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

PR 03-AUG-2000; 2000JP-0280988.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

DR MPI: 2001-376931/40.

DR N-PSDB; AAH65637.

PT Novel polynucleotides derived from Coryneform bacteria, for identifying

PT mutation point of a gene, measuring expression of a gene, analysing

PT expression profile or pattern of a gene and identifying homologous gene

PS Claim 17; SEQ ID NO: 4172; 246bp + Sequence Listing; English.

CC The present invention provides a number of nucleotide and protein

CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These

CC are useful for identifying the mutation point of a gene derived from a

CC mutant of coryneform bacterium, measuring expression amount and

CC analysing the expression profile or expression pattern of a gene derived

CC from Coryneform bacterium, and identifying a homologue of a gene derived

CC from coryneform bacterium. Coryneform bacteria are useful for producing

CC amino acids, nucleic acids, vitamins, saccharides and organic acids,

CC particularly L-lysine. The present sequence is a protein described

CC in the exemplification of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from the

CC European Patent Office.

CC Sequence 506 AA:

Query Match 31.5%; Score 615; DB 22; Length 506;

Best Local Similarity 32.2%; Pred. No. 1.8e-51;

Matches 148; Conservative 63; Mismatches 115; Indels 134; Gaps 6;

OY 29 GLVYNDFLIPGFIIDPDEVDTLSALTRKITKTPLISSPMQTVFEADAIMALMGCI 88

Db 21 gltfdvlllpdasdvpsvdstqltrnrlncpllsaaadvtlearmaigmartgh 80

OY 89 GFHNH-----CTPE----- 98

Db 81 gvlrhnlsiqeaaenvelvkrsesgmvtidpvcctpdmsiqevddlcarfrleglpvdea 140

OY 99 -----FOANEVRK----- 106

Db 141 gklvgictnrdrfseadmrrvaeytmpllvaaeeylkeqalalllsankvcklpliak 200

OY 107 -----VKREDKT-----LLCAAVGTREDDKYRDLDTLTAQGVDTYVD 144

Db 201 dgklvglltvcdfvkteqpnaskdasgrllvaagigtgeesfragaiaadgvdllvvd 260

OY 145 SSQGSNSVQIAMVHYIKORYPHLOVIGNVVTAQAOKNLIDAGVDELRYMGCGSICITQ 204

Db 261 sahabergvldmvrsvkksfpxvdlvgnlalreaaqaaleagadaikvgyigsstctr 320

OY 205 EVMACGRPGGTAVYKVAEFAARFVPIINDGGIQTIVGHVVKALALGASIVMMGSLAAT 264

Db 321 vvaqvgapqitlmeaavpahkayplladgymqfsgdlakalaagansvmslaga 380

OY 265 EAPGEYFSDGYRLKKYRGMSLDAM-----EKSSSOKRYFSEGDVKV--IAQVGS 314

Db 381 eapgetitngkykkyrgmngamqgrlgsekrtsykskdyfsgdvksedklypegie 440

OY 315 GSTIDKGSIQKFVYLLAGIOHCCODIGARSLVLRSMV 354

Db 441 grvfrgplgdllhngvgglraamgyltgsstleelnarf 480

RESULT 24

AAB80106
 ID AAB80106 standard; Protein; 506 AA.

AC AAB80106;

DT 30-APR-2001 (first entry)

DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:946.

KW Corynebacterium glutamicum; metabolic pathway protein; MP protein;

KW fine chemical production; microorganism; organic acid; nucleotide;

KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;

KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;

OS Corynebacterium glutamicum.

PN WO200100843-A2.

PD 23-JUN-2000; 2000WO-1B00923.

PR 25-JUN-1999; 99OS-0141031.

PR 01-JUL-1999; 99DE-1030476.

PR 02-JUL-1999; 99US-0142101.

PR 08-JUL-1999; 99DE-1031415.

PR 08-JUL-1999; 99DE-1031418.

PR 08-JUL-1999; 99DE-1031419.

PR 08-JUL-1999; 99DE-1031420.

PR 08-JUL-1999; 99DE-1031424.

PR 08-JUL-1999; 99DE-1031434.

PR 08-JUL-1999; 99DE-1031435.

PR 08-JUL-1999; 99DE-1031443.

PR 08-JUL-1999; 99DE-1031453.

PR 08-JUL-1999; 99DE-1031457.

PR 08-JUL-1999; 99DE-1031465.

PR 08-JUL-1999; 99DE-1031478.

PR 08-JUL-1999; 99DE-1031510.

PR 08-JUL-1999; 99DE-1031541.

PR 08-JUL-1999; 99DE-1031573.

PR 08-JUL-1999; 99DE-1031592.

CC useful in the desulfurisation of crude oil and petroleum products, and
CC for the clarification of soil and waste water contaminated by organic
CC sulphur compounds. Sequences AA97819-Y97829 represent the proteins
CC encoded by the genes of the *Pseudomonas* sp. WF505 benzothiophene oxidase
CC gene cluster.

XX	Sequence	489 AA;
SD		

Query Match	31.0%;	Score 605.5;	DB 21;	Length 489;
Best Local Similarity	31.3%;	Pred. No. 1.4e-50;		
Matches 149;	Conservative 64;	Mismatches 124;	Indels 139;	Gaps 6;

QY	30	LYVNDLFLLPEFDIFDEVDLFTALRRTKTLPLLSPPDQVTEYDMDIAAAMJIG	89
Db	8	ltfdvdlvlpafsqvlpkdsclakfsmnltnlplysaamdcvttearlalalagegig	67
QY	90	FIHNHTPEFOANEVRRVKFD	111
Db	68	lvhknltagqaaevakvkrkyesgvlrdpvltcthvrgymalsdqlgisgfpvdaqr	127
QY	112	-----KTL-----	115
Db	128	vvgivtgrdlrfenrydvpseimtgdrdlrltvpdgtlleakallnkhklierlvinsd	187
QY	116	-----CGAAVGTREDDKYRLDLTLTGADVVLIDS	145
Db	188	welkgiltvktkqtctfpmnaardasgrlrvgaavgyegteelcevalvayadavtcd	247
QY	146	SQGSNVYQIAMVHTIKQYRPHLOYIGGNVYTAOAKNLDAGVDGLRVMGCGSICITQE	205
Db	248	ahgnskvliervrwkkqnypldltvgnlaltgdaaraalaagadvavvrygipsictlrl	307
QY	206	VMACGRPOGTAVYVVAEAREFGVPIITADGICQVGVHVALAGASTVMGSLAATTE	265
Db	308	vaagvypgimavsvacalhgsvpyllisdgvyrgslakalaiaagasctmngsmfaglee	367
QY	266	APGEYFSDGVRLKKYRKMGSLDMAEKSSSQKRYFSEG-----DKVYIAQGVSGSIQ	318
Db	368	apgevlvyqrsyksygmgsigamqgsad-ryfgesttgnptdkl-vpegiegrvp	424
QY	319	DKSGIQKRVPLLINGIQHCODIARSLSVLRSMYSGELKTEKRTMSAQIEGVH	374
Db	425	yksjstsllygmagvvaasmgyccgclteemkn-----kaefvellttaglreshvh	475

Search completed: September 26, 2002, 08:26:52
Job time: 126 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OW protein - protein search, using sw model

Run on: September 26, 2002, 08:25:06 ; Search time 12.98 Seconds
(without alignments)
722.606 Million cell updates/sec

Title: US-09-853-918-30

Perfect score: 1955

Sequence: 1 MADYLISGTGVPEDELTA.....MSAQLDGCVGLHSYEKRLY 384

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PTOUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1655	84.7	514	4	US-08-925-230-8
2	1653	84.6	514	4	US-08-925-230-7
3	345	17.6	366	1	US-08-774-169-1
4	341	17.4	345	1	US-08-774-169-4
5	306.5	15.7	346	1	US-08-774-169-3
6	103	5.3	374	1	US-08-625-876-2
7	100	5.1	374	1	US-08-625-876-4
8	99	5.1	374	1	US-08-625-876-6
9	95	4.9	369	1	US-08-253-823-1
10	95	4.9	369	1	US-08-290-508-3
11	95	4.9	369	2	US-08-606-144-1
12	95	4.9	369	5	PCT-US94-02174-3
13	94.5	4.8	448	1	US-08-074-121-3
14	94.5	4.8	448	1	PCT-US94-06447-3
15	93.5	4.8	593	2	US-08-591-079-8
16	93.5	4.8	593	2	US-08-591-079-10
17	91.5	4.7	441	1	US-08-403-866-10
18	91	4.7	1052	4	US-09-255-502-7
19	90	4.6	2314	4	US-09-268-347-49
20	88	4.5	745	1	US-08-453-472-5
21	88	4.5	745	1	US-08-038-948-9
22	88	4.5	745	1	US-08-453-952-5
23	88	4.5	745	2	US-08-484-993B-43
24	88	4.5	745	2	US-08-862-903-5
25	88	4.5	745	2	US-08-484-158B-43
26	88	4.5	745	2	US-08-484-150A-43
27	88	4.5	745	2	US-08-480-150A-43

28	88	4.5	745	3	US-08-458-731-43	Sequence 43, Appl
29	88	4.5	745	3	US-08-149-223A-43	Sequence 43, Appl
30	87.5	4.5	1025	2	US-08-304-309-2	Sequence 2, Appl
31	87.5	4.5	1025	3	US-08-991-942-2	Sequence 2, Appl
32	87.5	4.5	1025	5	US-09-138-103-2	Sequence 4, Appl
33	87.5	4.5	1025	5	PCT-US95-04567-4	Sequence 4, Appl
34	86	4.4	251	2	US-08-846-762-11	Sequence 11, Appl
35	86	4.4	956	3	US-08-772-270A-8	Sequence 8, Appl
36	85.5	4.4	413	3	US-08-977-001-3	Sequence 3, Appl
37	85.5	4.4	682	1	US-08-441-119-2	Sequence 2, Appl
38	85.5	4.4	713	1	US-08-188-228-62	Sequence 62, Appl
39	85.5	4.4	713	1	US-08-332-643-56	Sequence 56, Appl
40	85.5	4.4	713	1	US-08-332-638-62	Sequence 62, Appl
41	85	4.3	323	6	5185254-4	Patent No. 5185254
42	84	4.3	1713	3	US-08-600-982-24	Sequence 24, Appl
43	84	4.3	1713	5	PCT-US94-10261A-24	Sequence 24, Appl
44	84	4.3	2511	4	US-09-261-907-2	Sequence 2, Appl
45	82	4.2	434	1	US-08-404-127-2	Sequence 2, Appl
46	82	4.2	434	2	US-09-041-011-2	Sequence 2, Appl
47	82	4.2	444	3	US-09-221-235-14	Sequence 14, Appl
48	82	4.2	444	3	US-09-221-928-14	Sequence 14, Appl
49	82	4.2	444	4	US-09-221-527-14	Sequence 14, Appl
50	82	4.2	444	4	US-09-221-236-14	Sequence 14, Appl
51	82	4.2	444	4	US-09-221-416-14	Sequence 14, Appl
52	82	4.2	444	4	US-09-221-245-14	Sequence 14, Appl
53	82	4.2	444	4	US-09-163-115-14	Sequence 14, Appl
54	82	4.2	444	4	US-09-221-528-14	Sequence 14, Appl
55	82	4.2	444	4	US-09-593-553-14	Sequence 14, Appl
56	82	4.2	444	4	US-09-221-237-14	Sequence 14, Appl
57	82	4.2	444	1	US-08-404-127-4	Sequence 4, Appl
58	82	4.2	445	2	US-09-041-011-4	Sequence 4, Appl
59	82	4.2	529	2	US-08-933-227-4	Sequence 4, Appl
60	82	4.2	540	2	US-08-368-882-34	Sequence 20, Appl
61	82	4.2	541	2	US-08-467-822-34	Sequence 34, Appl
62	82	4.2	541	2	US-08-447-154-19	Sequence 19, Appl
63	82	4.2	541	4	US-08-433-697-34	Sequence 34, Appl
64	82	4.2	541	4	US-08-466-248-34	Sequence 34, Appl
65	82	4.2	1360	4	US-09-393-265-2	Sequence 2, Appl
66	82	4.2	2509	1	US-08-469-005A-10	Sequence 10, Appl
67	81	4.1	423	2	US-08-715-554-2	Sequence 2, Appl
68	81	4.1	423	2	US-08-583-118-2	Sequence 2, Appl
69	81	4.1	456	2	US-08-679-635A-6	Sequence 6, Appl
70	80.5	4.1	341	1	US-08-314-309A-19	Sequence 19, Appl
71	80.5	4.1	524	3	US-08-557-210A-3	Sequence 3, Appl
72	80.5	4.1	539	3	US-08-557-210A-4	Sequence 4, Appl
73	80.5	4.1	539	3	US-08-557-210A-5	Sequence 5, Appl
74	80.5	4.1	1248	2	US-08-348-353-17	Sequence 17, Appl
75	80.5	4.1	1248	2	US-08-465-965-17	Sequence 17, Appl
76	80.5	4.1	1248	2	US-08-465-966-17	Sequence 17, Appl
77	80	4.1	275	6	5472855-5	Patent No. 5472855
78	80	4.1	275	6	US-08-431-387-7	Sequence 7, Appl
79	80	4.1	484	1	US-08-361-611-4	Sequence 4, Appl
80	80	4.1	484	1	US-08-565-655-4	Sequence 4, Appl
81	80	4.1	484	2	US-08-946-967-4	Sequence 4, Appl
82	80	4.1	691	1	PCT-US91-08442-2	Sequence 2, Appl
83	79.5	4.1	641	4	US-08-836-567-10	Sequence 10, Appl
84	79.5	4.1	3782	4	US-09-105-557-4	Sequence 4, Appl
85	79	4.0	275	5	PCT-US93-00418-3	Sequence 3, Appl
86	79	4.0	432	4	US-09-282-305-10	Sequence 10, Appl
87	79	4.0	947	1	US-09-228-986-73	Sequence 73, Appl
88	78.5	4.0	274	1	US-08-431-387-2	Sequence 2, Appl
89	78.5	4.0	274	2	US-08-865-203-7	Sequence 7, Appl
90	78.5	4.0	274	2	US-07-849-420-7	Sequence 7, Appl
91	78.5	4.0	274	4	US-09-253-854-7	Sequence 7, Appl
92	78.5	4.0	274	4	US-08-955-854-7	Sequence 7, Appl
93	78.5	4.0	350	1	US-07-923-260A-4	Sequence 4, Appl
94	78.5	4.0	375	1	US-08-121-714-5	Sequence 5, Appl
95	78.5	4.0	375	1	US-08-477-108A-5	Sequence 5, Appl
96	78.5	4.0	375	2	US-08-477-112-5	Sequence 5, Appl
97	78.5	4.0	375	2	PCT-US93-08332-5	Sequence 5, Appl
98	78.5	4.0	378	1	US-07-772-087-4	Sequence 4, Appl
99	78.5	4.0	379	2	US-08-845-295A-1	Sequence 1, Appl
100	78.5	4.0	379	3	US-09-140-933-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-08-925-230-8
; Sequence 8, Application US/08925230
; Patent No. 6147194
; GENERAL INFORMATION:
; APPLICANT: Collart, Frank
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,230
; FILING DATE: September 8, 1997
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 5,665,583
; FILING DATE: 12-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-925-230-8
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Query Match 84.7%; Score 1655; DB 4; Length 514;
Best Local Similarity 63.6%; Pred. No.2.6e-171;
Matches 327; Conservative 31; Mismatches 26; Indels 130; Gaps 1;

QY 1 MADYLLISGGGYPEDELTAQOOLFASADGLTYNDFILPGEFIDAEVDLTSAITPKIT 60
D 1 MADYLLISGGGYPEDELTAQOOLFASADGLTYNDFILPGEFIDAEVDLTSAITPKIT 60
QY 61 LKTPILISSPMDYTEADMAIAMLGMGIGFIHNCTPEFOANEVRKVKKFD----- 111
D 61 LKTPILISSPMDYTEADMAIAMLGMGIGFIHNCTPEFOANEVRKVKKFD----- 111
QY 112 ----- 111
D 112 ----- 111
QY 181 KREDLVVAPAGITLKEANELLQSKRGKLPIVENDELVAIARTDLKKNRDYPLASKDA 240
QY 112 -KTLGGAAGVTRDDKRYRLDLTQAGVDYIVLSSQSGNSVYQIAWHYKOKYPHLOVI 170
D 241 KKOLLGGAIGTHEDDKRYRLDLTQAGVDYIVLSSQSGNSVYQIAWHYKOKYPHLOVI 300
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QY 171 GGNVYTAQAQKNLIDAGVDGLRVMGCGSICITQEVWACGRPGCTAVYKVAEYARRFCVP 230
D 301 GGNVYTAQAQKNLIDAGVDALRVMGCGSICITQEVWACGRPGCTAVYKVAEYARRFCVP 360
QY 231 IADGGIOYGVHVKALALGASTVMGSLAATTEAPGEYFSDGIRLKKYRGMGSLDAM 290
D 361 IADGGIOYGVHVKALALGASTVMGSLAATTEAPGEYFSDGIRLKKYRGMGSLDAM 420
QY 291 EKSSSQKRYFSEGDYKVIAGVSGSIODKSGIOKEFVYLIAGIOHGCODIGARSLVLR 350
D 421 DKHLSSQKRYFSEADKIVAGVSGAVODKSGIHKFVYLIAGIOHGCODIGARSLVLR 480
QY 351 SMWISGELKFKRRTMSAQIEGVGHSHYKRLY 384
D 481 AMWISGELKFKRRTSSNOVGVGHSHYKRLY 514
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RESULT 2
US-08-925-230-7
; Sequence 7, Application US/08925230
; Patent No. 6147194
; GENERAL INFORMATION:
; APPLICANT: Collart, Frank
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,230
; FILING DATE: September 8, 1997
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 5,665,583
; FILING DATE: 12-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-925-230-7
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Query Match 84.6%; Score 1653; DB 4; Length 514;
Best Local Similarity 63.8%; Pred. No.4.3e-171;
Matches 328; Conservative 29; Mismatches 27; Indels 130; Gaps 1;

QY 1 MADYLLISGGTYPEDELTAQOOLFASADGLTYNDFILPGEFIDAEVDLTSAITPKIT 60
D 1 MADYLLISGGTYPEDELTAQOOLFASADGLTYNDFILPGEFIDAEVDLTSAITPKIT 60
QY 61 LKTPILISSPMDYTEADMAIAMLGMGIGFIHNCTPEFOANEVRKVKKFD----- 111
D 61 LKTPILISSPMDYTEADMAIAMLGMGIGFIHNCTPEFOANEVRKVKKFD----- 111
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Db 61 LKTPLVSSPMDTVEAGAAIAMAALTGIGFIHNNCTPEFOANEVRKVKYEGGTTDPVY 120
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Qy 112 ----- 111
Db 181 KREDLVAPRSITLKEANEILLQRSKKGLPIVNEDELVAIARTDLKKNRDYPLASKDA 240
Qy 112 ----- 111
Db 112 -KTLGCAAVGTREDDKRLDLITAGVDYIVLDSOGNSVQIAMVHYIKQKTYHLOYI 170
Db 241 KKOLLGGAIGITHEDDKRLDLAAGVDVYVLLDSSQGSIFQIMWIKYIKKYPNLOYI 300
Qy 171 GGNVYTAQAOKNLIDAGVDGLRVGMCSSICTOEVMACGRPGTAAYVYKVAEYARFGVP 230
Db 301 GGNVYTAQAOKNLIDAGVDALRVGMCSSICTOEVLACGRQAATAVYKVEYARFGVP 360
Qy 231 IADGGIQTGVHVKALALGASTVMGSLAATTEAPGEYFFSDGVRLLKRYRGMGLDAM 290
Db 361 VYADGIGNVGHIAKALALGASTVMGSLAATTEAPGEYFFSDGIRLLKRYRGMGLDAM 420
Qy 291 EKSSSOKRPFSEGDVKVIAQVSGSIQDKGSIQKFFVPIYLLGIQHCODIGARSLSVLR 350
Db 421 DKHLSSQNRPFSEADKIKVAGVSGAVQDKGSIHKFVYLLAGIQHSCODIGAKSLTOVR 480
Qy 351 SMVYSGELKFEKRTMSAOIEGGVHGLHSEKRLY 384
Db 481 AMVYSGELKFEKRTSSAQVEGSHLHSEKRLF 514

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RESULT 3
US-08-774-169-1
; Sequence 1, Application US/08774169
; Patent No. 5756332

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GENERAL INFORMATION:

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APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL GUANOSINE MONOPHOSPHATE REDUCTASE
NUMBER OF SEQUENCES: 4

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774.169
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0182 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

```

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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:

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; LIBRARY: Consensus
; CLONE: Consensus
US-08-774-169-1

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Query Match 17.6%; Score 345; DB 1; Length 366;
Best Local Similarity 29.3%; Pred. No. 4.4e-29;
Matches 97; Conservative 65; Mismatches 145; Indels 24; Gaps 6;

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Qy 30 LTYNDFLLPGTIDFA-DEVDTLSALTRKITLKT-----PLISSPMDTVEADMAIAMAAL 84
Db 28 LDFKVLRLPRKRTLSKSSEVDLTRSFSEFRNKQTYSGVPIIAANMDYVGFEMAKVLYC 87
Qy 85 MGIGFIHNNCT----PEFOANEVRKVKFKDITLGAAGVREDDKRLDLITQAA--GV 138
Db 88 FSLFPAVAKHSHLYWQMEFAGNPDCLHEL-----MASSGSSGDFQLBILIAITQY 141
Qy 139 DVIYLDSSQNSVQIAMVHYIKQYPHLQVIGVNVYTAQAOKNLIDAGVDGLRVGMC 198
Db 142 KYICLDVANGVSEHVEFEVKDYKRFPPOHTIMAGVNVYTGEMVEEILSGADIITKVGIGPG 201
Qy 199 SICITQEVYMACGRPGTAAYVYKVAEYARFGVPIIADGGIQTGVHVKALALGASTVMG 258
Db 202 SVCTTRKKTGVGYPOLSAVMECADAHLKGHIISDGCSCPGDVAKAFAGADVYMLGG 261
Qy 259 LIAATTEAPGEYFFSDGVRLLKRYRGMGLDAMEKSSSOKRPFSEGDVKVIAQVSGSIQ 318
Db 262 MLAGHSESGELIENDKRYKLFYGMSSBMAKKYKAGVAAEY-----RASEGKTVYRP 314
Qy 319 DKGSIQKFFVPIYLLAGIQHCODIGARSLSVL 349
Db 315 FKGDVEHTIRDLIGIRSTCTFYGAAKLEL 345

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RESULT 4
US-08-774-169-4
; Sequence 4, Application US/08774169
; Patent No. 5756332

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GENERAL INFORMATION:

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APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: A NOVEL GUANOSINE MONOPHOSPHATE REDUCTASE
NUMBER OF SEQUENCES: 4

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/774.169
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0182 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid

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; LIBRARY: Consensus
; CLONE: Consensus
US-08-774-169-1

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,876
FILING DATE: 01-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-95947
FILING DATE: 30-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-146186
FILING DATE: 13-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: PF-1612
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-625-876-6

Query Match 5.18; Score 99; DB 1; Length 374;

Best Local Similarity 21.98; Pred. No. 0.026;
Matches 77; Conservative 46; Mismatches 135; Indels 94; Gaps 17;

QY 8 GGTGVEDEGLTAAQLFASADGLTYNDLPLPGFIDPLADEVDLTSALTRKTLTKPLIS 67
DB 36 GGFNYIA--GASGDEWTKRANBRAMKHLXPRLAQDVEAPDSTELLGHKI--KAPFIM 91
QY 68 SPM-----DVTADADAIAMALMGIGFTIHNTPEQANEVKKVFKFDKLLCGAVG 121
DB 92 APIAHGLAHTTKKAGTAAVSEGTIMISAYSATFE--EISE-----GNGG 139
QY 122 TR-----EDDKYRLDLTGAGVD-----VIVDSS--QGN-----VYQIANYHI 160
DB 140 PRWQIYMAKDDQNRDLIDGAKSDGATAILITLADSTVSGNRDVKKFFYPGMP--I 197
QY 161 KQKY-----PHLYQVIGNVVTAQAQKMLIDAGVDGLR-----VGMGC 197
DB 198 VQYLRGTAEGLSDNIYASKOKISPRDIEIAHSGLPVFKGIQHPEDADMAIKAGA 257
QY 198 GSICITQEVMAAGRPQGTAVYK-----VAEYARREGVPIIADGGIQTGVHVKAL 247
DB 258 SGIVWSNH---GARQ---IYEAQSFDTLPALAEVKN--RVPIVFSGVRGGEHAKAL 309
QY 248 ALGASTVMGSLAATTEAPG-----EYFSDGVRLKKYRGMSIDAME 291
DB 310 ASGADVVALGRPVLFGLALGSGMGAYSLVDYFQKDLTRVMQLTGSQVVEDLK 361

RESULT 9

US-08-253-823-1
Sequence 1, Application US/08253823

Patent No. 5541094

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: GLYCOLATE OXIDASE PRODUCTION

NUMBER OF SEQUENCES: 1

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM

OPERATING SYSTEM: MICROSOFT WINDOWS V3.0

SOFTWARE: MICROSOFT WORD V2.0C

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,823

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/085,488
FILING DATE: JULY 1, 1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-253-823-1

Query Match

Best Local Similarity 4.98; Score 95; DB 1; Length 369;
Matches 47; Conservative 23; Mismatches 63; Indels 44; Gaps 8;

QY 120 VGTRED--KTR-----LDLTQAGVVIYLD---SSQGSNVYQIANYHI-----KQ 162
DB 161 LGREADIKRRFVLPPLTLTKNEGIDLGKMDKANDSLSSVAGQIDRSLSKKDVAWLQ 220
QY 163 KYPHLYQVIGNVVTAQAQKMLIDAGVDGLRV--GMGC-----GSICITQEVN--ACGRP 212
DB 221 TITSLPLVAGVITAEDARLAVOHGAGGITYSNHGAQOLDYVPTATIALEEVYKNAQGR- 279
QY 213 QGTAVVYKAEYARREGVPIIADGGIQTGVHVKALALGASTVMGSLAATTEAPGE 269
DB 280 -----IPVFLDGVRRGTDVFKALALGAGVFIGRPVVFSLAAGE 320

RESULT 10

US-08-290-508-3
Sequence 3, Application US/08290508

Patent No. 5693490

GENERAL INFORMATION:

APPLICANT: PAYNE, MARK S.

APPLICANT: ANTON, DAVID L.

APPLICANT: DICOSTINO, ROBERT

TITLE OF INVENTION: Production of glycolate oxidase

TITLE OF INVENTION: in methylotrophic yeast

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS

ADDRESSEE: AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: U.S.A.

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH 1.0 MB

COMPUTER: MACINTOSH

OPERATING SYSTEM: MACINTOSH SYSTEM, 6.0

SOFTWARE: MICROSOFT WORD, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,508

FILING DATE: 15-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/025,495

FILING DATE: 03-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: GALLEGO, R. THOMAS

REGISTRATION NUMBER: 32,692

REFERENCE/DOCKET NUMBER: CR-9271

TELEPHONE: 302-892-7342

TELEFAX: 302-892-7949

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 369 amino acids

TYPE: amino acid

Query match 4.98; Score 95; DB 2; Length 369;

ADDRESSEE: Fish & Richardson

STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: California
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/074,121
FILING DATE: 08-JUN-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Ventler, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: 05938/043001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-5277
TELEFAX: (415) 854-0875
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-074-121-3

Query Match 4.88; Score 94.5; DB 1; Length 448;

Best Local Similarity 21.28; Pred. No. 0.11;

Matches 73; Conservative 41; Mismatches 120; Indels 111; Gaps 13;

QY 45 IADVLTSLTRKTLTKPLISSPMDVTEADMAIAMLGIGFIHNCPTPEQANE 103
DB 44 LADFTVCIGRPVSKSYLNIPAI-----ISAETIGAVAIHPGYFLSEN-----ANF 91
QY 104 VRVKKFEDKTLGCAAVGTREDKRYRLDLTQAGVDVIVLDSQGSNSVYOIAVNHVYIKOK 163
DB 92 AEQVER-----SGFIFIGPK 106
QY 164 YPHLOVIGNVVTAQAOKNLIDAGVDGLRVGMCSCICTQEVYMACRPGGTAVYKVAEY 223
DB 107 AETIRLMGDKVSAIAAMK-----KAGVPC-----VPGSDGPLGDDMKNRAI 148
QY 224 ARRGVPII--ADGGIQTVG--HYVKALALGASTVMGSLAATTEAPGEYFFS--DGVRLK 279
DB 149 AKRIGFVPIIKASGGGGRGRRVVRGDAELAQISIM-----TRAARAAFSNDVYME 201
QY 280 KY-----RGMG--SLDAMEKSSSSQKRYFSEGDVKYIAQVSGSIODKSIQK 325
DB 202 KYLENPRHVEIOVLADGGNAIYLAERDCSMORRH-----QKVVEEAPAPGITPE 251
QY 326 FVPYLLAGIOHGGODIGARSLSVLRSMYSGELKFEKRTMSAQIE 370
DB 252 LRRYIGERCACACVDIGYRGAGTFFELFENGEEFYFIEMNTRIOVE 296

RESULT 14
PCT-US94-06447-3

Sequence 3, Application PC/US9406447
GENERAL INFORMATION:
APPLICANT: Calgene, Inc.
TITLE OF INVENTION: Methods and Compositions for Modulating
TITLE OF INVENTION: Lipid Content of Plant Tissues
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weill, Gotshal & Manges
STREET: 2882 Sand Hill Road, Suite 280
CITY: Menlo Park
STATE: California

COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06447
FILING DATE: 06-JUN-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Ventler, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE-097/MO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-06447-3

Query Match 4.88; Score 94.5; DB 5; Length 448;

Best Local Similarity 21.28; Pred. No. 0.11;

Matches 73; Conservative 41; Mismatches 120; Indels 111; Gaps 13;

QY 45 IADVLTSLTRKTLTKPLISSPMDVTEADMAIAMLGIGFIHNCPTPEQANE 103
DB 44 LADFTVCIGRPVSKSYLNIPAI-----ISAETIGAVAIHPGYFLSEN-----ANF 91
QY 104 VRVKKFEDKTLGCAAVGTREDKRYRLDLTQAGVDVIVLDSQGSNSVYOIAVNHVYIKOK 163
DB 92 AEQVER-----SGFIFIGPK 106
QY 164 YPHLOVIGNVVTAQAOKNLIDAGVDGLRVGMCSCICTQEVYMACRPGGTAVYKVAEY 223
DB 107 AETIRLMGDKVSAIAAMK-----KAGVPC-----VPGSDGPLGDDMKNRAI 148
QY 224 ARRGVPII--ADGGIQTVG--HYVKALALGASTVMGSLAATTEAPGEYFFS--DGVRLK 279
DB 149 AKRIGFVPIIKASGGGGRGRRVVRGDAELAQISIM-----TRAARAAFSNDVYME 201
QY 280 KY-----RGMG--SLDAMEKSSSSQKRYFSEGDVKYIAQVSGSIODKSIQK 325
DB 202 KYLENPRHVEIOVLADGGNAIYLAERDCSMORRH-----QKVVEEAPAPGITPE 251
QY 326 FVPYLLAGIOHGGODIGARSLSVLRSMYSGELKFEKRTMSAQIE 370
DB 252 LRRYIGERCACACVDIGYRGAGTFFELFENGEEFYFIEMNTRIOVE 296

RESULT 15

US-08-591-079-8

Sequence 8, Application US/08591079
Patent No. 5972899
GENERAL INFORMATION:
APPLICANT: Zychlinsky, Arturo
APPLICANT: Chen, Yajing
TITLE OF INVENTION: Apoptosis Induced by Shigella Ipab
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812


```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591.079
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 15661-20017.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0764
TELEX: 90-4030 MRSNFOERSM
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-079-8
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Query Match 4.8%; Score 93.5; DB 2; Length 593;
Best Local Similarity 19.6%; Pred. No. 0.21;
Matches 72; Conservative 57; Mismatches 124; Indels 115; Gaps 17;
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```
QY 47 DEVDLTSLTRITLTKPLISSPMDVTVEADMAIMALMGIGIGFIHNCTPEFOANEVRK 106
DB 248 DNLISNVARLTMLAMFETLVGNKTESLQNDLALFNALDEGQAEMEKKSAEFQ-BETRK 306
QY 107 VKRFDKTLIC-GAAGTRDDKRYRLDLT-----QAGVDYIYLD--- 144
DB 307 ABEETNIMCICKIVLGA-----LRTIVSVAAVFTGASLAAVGLAVMADEIV 357
QY 145 -SSQGNSTYQIA---MWHYIKOKYPHLOVIGGNVNTAAQKNLIDAGVD-----GLR 192
DB 358 KATGVSFIOALNPLMEHVLK---PLMELIG-----KAITTALBGLGYDKKTAEMAGSI 409
QY 193 VGMGCGSICITQEVN-----ACGRPGGTAVYK---VAEYARFQVPIIA 233
DB 410 VCAIYVAIAMVAVIVVAVVGAAGAAGLGNALSKMMGETIKKLVPNVLKQLAONGSKLFT 469
QY 234 DG-----GIOT-----VGHVVKALALG-----ASTVMGSLIA 261
DB 470 QGMQRTISGLGNVSKMGLOTNALSKELVGNLTKVALLGMEVYNTAAQSAGVABGVFIK 529
QY 262 ATTEAPGEYFFSDGVRLKRYRGMSLIDAMEKSSSSQKRYFSEGDY--KIAQGVSGSID 319
DB 530 NASEALADFM-----LARF-----AMDQIQMLKQSEVETIGENOKVTAELOKMASSAVQO 579
QY 320 KGSIOKEV 327
DB 580 NADASRFI 587
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```
RESULT 16
US-08-591-079-10
; Sequence 10, Application US/08591079
; Patent No. 5972899
; GENERAL INFORMATION:
; APPLICANT: Zychlinsky, Arturo
; APPLICANT: Chen, Yajing
; TITLE OF INVENTION: Apoptosis Induced by Shigella Ipab
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW
; CITY: Washington
; STATE: DC
```

```
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591.079
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Livnat, Shmuel
REGISTRATION NUMBER: 33,949
REFERENCE/DOCKET NUMBER: 15661-20017.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0764
TELEX: 90-4030 MRSNFOERSM
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-591-079-10
```

```
Query Match 4.8%; Score 93.5; DB 2; Length 593;
Best Local Similarity 19.6%; Pred. No. 0.21;
Matches 72; Conservative 57; Mismatches 124; Indels 115; Gaps 17;
```

```
QY 47 DEVDLTSLTRITLTKPLISSPMDVTVEADMAIMALMGIGIGFIHNCTPEFOANEVRK 106
DB 248 DNLISNVARLTMLAMFETLVGNKTESLQNDLALFNALDEGQAEMEKKSAEFQ-BETRK 306
QY 107 VKRFDKTLIC-GAAGTRDDKRYRLDLT-----QAGVDYIYLD--- 144
DB 307 ABEETNIMCICKIVLGA-----LRTIVSVAAVFTGASLAAVGLAVMADEIV 357
QY 145 -SSQGNSTYQIA---MWHYIKOKYPHLOVIGGNVNTAAQKNLIDAGVD-----GLR 192
DB 358 KATGVSFIOALNPLMEHVLK---PLMELIG-----KAITTALBGLGYDKKTAEMAGSI 409
QY 193 VGMGCGSICITQEVN-----ACGRPGGTAVYK---VAEYARFQVPIIA 233
DB 410 VCAIYVAIAMVAVIVVAVVGAAGAAGLGNALSKMMGETIKKLVPNVLKQLAONGSKLFT 469
QY 234 DG-----GIOT-----VGHVVKALALG-----ASTVMGSLIA 261
DB 470 QGMQRTISGLGNVSKMGLOTNALSKELVGNLTKVALLGMEVYNTAAQSAGVABGVFIK 529
QY 262 ATTEAPGEYFFSDGVRLKRYRGMSLIDAMEKSSSSQKRYFSEGDY--KIAQGVSGSID 319
DB 530 NASEALADFM-----LARF-----AMDQIQMLKQSEVETIGENOKVTAELOKMASSAVQO 579
QY 320 KGSIOKEV 327
DB 580 NADASRFI 587
```

```
RESULT 17
US-08-403-866-10
; Sequence 10, Application US/08403866
; Patent No. 5643779
; GENERAL INFORMATION:
; APPLICANT: Ehrlich, Stanislaw
; APPLICANT: Godon, Jean-Jacques
; APPLICANT: Renault, Pierre
; TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
; TITLE OF INVENTION: synthase from Lactococcus and its applications
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
```


TELEPHONE: (202) 861-3000
 TELEFAX: (202) 822-0944
 TELETYPE: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 745 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-038-948-9

Query Match 4.5%; Score 88; DB 1; Length 745;
 Best Local Similarity 19.1%; Pred. No. 1.2;
 Matches 66; Conservative 57; Mismatches 108; Indels 114; Gaps 18;

QY 93 HNCITPEQANEVRKVKFEDTLLCGAAGVGTREDKRYRLDLTQAGVD----- 139
 DB 442 HALMTDPPSKISDSEFRMTVKCSYS-----RNDMLNINVESLTPPVASVKLGP 492
 QY 140 -VIVLDSOGNSVYQ-----IAMVHYIKOK-YPHLOVIGN-----VVTAAQAKNLID 185
 DB 493 FTLLQSYPNSSYQPPGENEYPLVRFLRQPIYMEVRLNRDNPNIKLVLDCCMASTMD 552
 QY 186 AG-----VDGLRVGMCGSICITQEVNACGRPGGTAYKVAEVARRGVPIADGGI 237
 DB 553 PDSEFQMNVVVDCAYDL-----DNYQTTFHPVGSSVTHPDHY-QREDMKAF--F 600
 QY 238 QTGVHVKALALAGASTVMGSLA-----ATTEA-----PGE- 269
 DB 601 VSEAHVLSLVYFHCALICNRLSPDPLCSVTCPVSSRRHRATGATEAKMTVSLPGPI 660
 QY 270 YFSDGVRLKKRYGMSLDAMEKSSSQKRYFSEGDVKVIAQVSGSIDQKGIQKFPVY 329
 DB 661 LLLSD-----SSFRGVGSSDLKAGSSGSEKSRSETEEV-----GSRGAMDTKG-----H 706
 QY 330 LINGIHCODIGARSLSVLRSMYSGELK-----FEKRTMS 366
 DB 707 KTAG-----DVGSKAVAAVA--FAGVVATLIGFIYLYLEKRTVS 743

RESULT 22
 US-08-453-952-5
 ; Sequence 5, Application US/08453952
 ; Patent No. 5672488
 ; GENERAL INFORMATION:
 ; APPLICANT: DEAN, JURRIEN
 ; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
 ; TITLE OF INVENTION: BASED ON ALLOIMMUNIZATION WITH ZONA PELLUCIDA
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/453,952
 ; FILING DATE: 30-May-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/038,948
 ; FILING DATE: 26-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/930,462

FILING DATE: 20-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/364,379
 FILING DATE: 12-JUN-1989
 ATTORNEY/AGENT INFORMATION:
 NAME: DOROTHY R. AOTH
 REGISTRATION NUMBER: 36,434
 REFERENCE/DOCKET NUMBER: 2026-4032 USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 ;
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 745
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: human
 ; STRAIN:
 ; INDIVIDUAL ISOLATE:
 ; DEVELOPMENTAL STAGE:
 ; HAPLOTYPE:
 ; CELL TYPE:
 ; TISSUE TYPE:
 ; CELL LINE:
 ; ORGANELLE:
 ; FEATURE:
 ; NAME/KEY: 2P2
 ; LOCATION:
 ; IDENTIFICATION METHOD:
 ; OTHER INFORMATION: human 2P2 protein
 ;
 ; US-08-453-952-5

Query Match 4.5%; Score 88; DB 1; Length 745;
 Best Local Similarity 19.1%; Pred. No. 1.2;
 Matches 66; Conservative 57; Mismatches 108; Indels 114; Gaps 18;

QY 93 HNCITPEQANEVRKVKFEDTLLCGAAGVGTREDKRYRLDLTQAGVD----- 139
 DB 442 HALMTDPPSKISDSEFRMTVKCSYS-----RNDMLNINVESLTPPVASVKLGP 492
 QY 140 -VIVLDSOGNSVYQ-----IAMVHYIKOK-YPHLOVIGN-----VVTAAQAKNLID 185
 DB 493 FTLLQSYPNSSYQPPGENEYPLVRFLRQPIYMEVRLNRDNPNIKLVLDCCMASTMD 552
 QY 186 AG-----VDGLRVGMCGSICITQEVNACGRPGGTAYKVAEVARRGVPIADGGI 237
 DB 553 PDSEFQMNVVVDCAYDL-----DNYQTTFHPVGSSVTHPDHY-QREDMKAF--F 600
 QY 238 QTGVHVKALALAGASTVMGSLA-----ATTEA-----PGE- 269
 DB 601 VSEAHVLSLVYFHCALICNRLSPDPLCSVTCPVSSRRHRATGATEAKMTVSLPGPI 660
 QY 270 YFSDGVRLKKRYGMSLDAMEKSSSQKRYFSEGDVKVIAQVSGSIDQKGIQKFPVY 329
 DB 661 LLLSD-----SSFRGVGSSDLKAGSSGSEKSRSETEEV-----GSRGAMDTKG-----H 706
 QY 330 LINGIHCODIGARSLSVLRSMYSGELK-----FEKRTMS 366
 DB 707 KTAG-----DVGSKAVAAVA--FAGVVATLIGFIYLYLEKRTVS 743

RESULT 23
 US-08-484-993B-43
 ; Sequence 43, Application US/08484993B
 ; Patent No. 5837497
 ; GENERAL INFORMATION:
 ; APPLICANT: Harris Ph.D., Jeffrey D.
 ; APPLICANT: Hsu, Kuang T.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:25:31 ; Search time 21 Seconds
(without alignments)
1757.062 Million cell updates/sec

Title: US-09-853-918-30

Perfect score: 1955
Sequence: 1 MADYLISGGTGVPEDELTA.....MSAQIEGVHGLHSYKRLY 384

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR-71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1858	95.0	514	1 A35566	IMP dehydrogenase
2	1655	84.6	514	1 B31997	IMP dehydrogenase
3	1653	84.6	514	1 A31997	IMP dehydrogenase
4	1640	83.9	514	1 UT0565	IMP dehydrogenase
5	1348.5	69.0	537	1 S41064	IMP dehydrogenase
6	1271.5	65.0	537	1 S59508	IMP dehydrogenase
7	1245.5	63.7	524	1 S50890	IMP dehydrogenase
8	1238.5	63.4	523	1 S59402	IMP dehydrogenase
9	1233.5	63.1	523	1 S48997	IMP dehydrogenase
10	1094.5	56.0	512	1 A55407	IMP dehydrogenase
11	1087.5	55.6	514	1 A38668	IMP dehydrogenase
12	1076.5	55.1	524	1 T40127	IMP dehydrogenase
13	1039.5	53.2	499	1 T32709	IMP dehydrogenase
14	1016	52.0	502	1 P86298	IMP dehydrogenase
15	1007.5	51.5	503	1 JC4999	IMP dehydrogenase
16	691.5	35.4	403	1 S53477	IMP dehydrogenase
17	674	34.5	485	1 D97232	IMP dehydrogenase
18	654.5	33.5	485	1 G81308	IMP dehydrogenase
19	649	33.2	490	1 H70473	IMP dehydrogenase
20	649	33.2	509	2 JC7305	IMP dehydrogenase
21	641.5	32.8	482	2 C72264	IMP dehydrogenase
22	632	32.3	489	2 H83173	IMP dehydrogenase
23	629	32.2	485	2 B82558	IMP dehydrogenase
24	628	32.1	485	2 D83652	inositol-monophosp
25	626.5	32.0	488	2 DEBSMP	IMP dehydrogenase
26	626	32.0	487	2 F81906	IMP dehydrogenase
27	625	31.9	487	1 H81109	IMP dehydrogenase
28	624.5	31.4	488	1 S23226	IMP dehydrogenase
29	613.5	31.4	521	1 T17196	IMP dehydrogenase

30	613	31.4	488	2 C89805	inositol-monophosp
31	610.5	31.2	529	1 H70736	IMP dehydrogenase
32	606.5	31.0	500	1 F75342	IMP dehydrogenase
33	601	30.7	404	1 E70218	IMP dehydrogenase
34	600.5	30.7	488	1 DECIIP	IMP dehydrogenase
35	600.5	30.7	488	2 B91050	IMP dehydrogenase
36	600.5	30.7	488	2 G85894	IMP dehydrogenase
37	600.5	30.7	529	1 S72823	IMP dehydrogenase
38	600	30.7	489	2 C82282	IMP dehydrogenase
39	599.5	30.7	357	1 B81701	probable IMP dehyd
40	597.5	30.6	488	2 AE1419	inosine-monophosph
41	597.5	30.6	488	2 AF1794	inosine-monophosph
42	597.5	30.6	490	2 AE0820	IMP dehydrogenase
43	589.5	30.2	487	2 AC0349	IMP dehydrogenase
44	586.5	30.0	488	2 H64055	IMP dehydrogenase
45	585.5	29.9	499	2 AC3621	inosine-5'-monopho
46	577	29.5	493	1 JC4372	IMP dehydrogenase
47	574.5	29.4	492	2 C95260	inosine-5'-monopho
48	574.5	29.4	492	2 F98125	IMP dehydrogenase
49	574	29.4	481	1 E64623	IMP dehydrogenase
50	572	29.3	481	1 H71890	IMP dehydrogenase
51	570.5	29.2	493	2 D86652	IMP dehydrogenase
52	565	28.9	487	2 H87449	inosine-5'-monopho
53	552.5	28.3	503	2 F97434	guab protein (AE27
54	523.5	26.8	484	1 B69056	IMP dehydrogenase
55	516	26.4	473	2 AB2653	inosine-5'-monopho
56	505	25.8	496	1 G64501	IMP dehydrogenase
57	504.5	25.8	157	1 S78078	IMP dehydrogenase-
58	491	25.1	485	2 E75015	IMP dehydrogenase
59	490.5	25.1	486	1 E71456	IMP dehydrogenase
60	490	25.1	485	1 JC4998	IMP dehydrogenase
61	487.5	24.9	527	2 F84256	inosine monophosph
62	484	22.2	246	1 C72109	IMP dehydrogenase
63	434	22.2	246	2 D86512	inosine 5'-monopho
64	394	20.2	444	1 D72631	probable IMP dehyd
65	384.5	19.7	503	2 A58910	IMP dehydrogenase
66	375.5	19.2	502	1 AE1091	inosine monophosph
67	373.5	19.1	502	2 AD1455	inosine monophosph
68	354	18.1	347	2 F82490	GMP reductase VC40
69	348	17.8	479	1 C70664	IMP dehydrogenase
70	339	17.3	325	1 A71887	probable GMP reduct
71	335	17.1	327	1 F64626	probable GMP reduct
72	335	17.1	327	2 D97326	GMP reductase [lmp
73	335	17.1	345	1 B32902	GMP reductase [lmp
74	331.5	17.0	328	2 G98012	GMP reductase [lmp
75	325.5	16.7	328	2 A05145	conserved hypotnet
76	325	16.6	326	1 C70015	probable GMP reduct
77	324	16.6	478	1 T44751	IMP dehydrogenase
78	320.5	16.4	347	2 A80416	GMP reductase [lmp
79	318	16.3	347	2 D90642	GMP reductase [lmp
80	318	16.3	347	2 D85493	GMP reductase [lmp
81	317	16.2	347	1 H64732	GMP reductase [lmp
82	312	16.0	358	1 T03917	GMP reductase [lmp
83	310	15.9	329	2 A86768	GMP reductase [lmp
84	296	15.1	325	2 B89909	hypothetical prote
85	295.5	15.1	347	2 AD0520	GMP reductase [lmp
86	289.5	14.8	349	2 A84954	GMP reductase [lmp
87	247.5	12.7	387	2 AC1813	GMP reductase [lmp
88	245.5	12.6	387	1 S75050	IMP dehydrogenase
89	188.5	9.6	375	1 G70736	IMP dehydrogenase-
90	168.5	8.6	370	1 D66957	probable inosine-5-
91	168.5	8.6	375	1 S72812	IMP dehydrogenase-
92	157	8.0	383	2 D86781	L-lactate oxidase
93	152	7.8	274	2 E69521	2-oxopropene dio
94	151	7.7	310	2 H97338	conserved hypotnet
95	148.5	7.6	321	2 A87668	hypothetical prote
96	148.5	7.6	315	2 B83676	conserved hypotnet
97	140	7.2	325	2 D87619	hypothetical prote
98	138	7.1	322	2 C70700	hypothetical prote
99	136.5	7.0	309	2 AB1346	hypothetical prote
100	136	7.0	311	2 A87444	conserved hypotnet

ALIGNMENTS

```
RESULT 1
A35566
IMP dehydrogenase (EC 1.1.1.205) I - human
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1990 #sequence_rev1sion 21-Sep-1990 #text_change 05-May-2000
C:Accession: A35566
J:Ratsmeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.
R: Biol. Chem. 265, 5292-5295, 1990
A:Title: Two distinct cDNAs for human IMP dehydrogenase.
A:Reference number: A35566; MUID:90203022
A:Accession: A35566
A:Molecule type: mRNA
A:Residues: 1-514 <RNA>
A:Cross-references: GB:J05272; NID:q186393
A:Note: the sequence in GenBank entry HUMIMPH, release 103, (PID:q307067) has 273-Phe, 2
A:Comment: mRNA for IMP dehydrogenase I predominated in normal leukocytes, whereas that
C:Genetics:
A:Gene: GDB:IMPDH1; SWSS2608
A:Cross-references: GDB:128085; OMIM:146690
A:Map position: 7q31.3-7q32
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolo
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
F:117-168/Domain: IMP dehydrogenase amino-terminal homology <IDHM>
F:184-332/Domain: CBS homology <CBS1>
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted

Query Match 95.0%; Score 1858; DB 1; Length 514;
Best Local Similarity 73.9%; Pred. No. 9, 6e-129;
Matches 380; Conservative 1; Mismatches 3; Indels 130; Gaps 1;

Db 1 MADYLSGCGTGYPPEDGTLTAQOLFASADGLTYNDFLTPGFIDEVDTLSALTRKIT 60
1 MADYLSGCGTGYPPEDGTLTAQOLFASADGLTYNDFLTPGFIDEVDTLSALTRKIT 60
OY 61 LKTPLISSPMDVTYTDADMAIAMLAMGIGIFIHNCPTPEOFANEVRKYKFD----- 111
1 LKTPLISSPMDVTYTDADMAIAMLAMGIGIFIHNCPTPEOFANEVRKYKFD----- 111
Db 61 LKTPLISSPMDVTYTDADMAIAMLAMGIGIFIHNCPTPEOFANEVRKYKFD----- 111
OY 112 ----- 111
112 ----- 111
Db 121 LSPSHVGVDLVLEAKMRHGFSGIPITETGTGMSKLVGIVTSRDIDFLAEKDHDTLLSEVMT 180
OY 112 ----- 111
112 ----- 111
Db 181 PRIELVVAAPAGVTLKEANELLORSKKGKLPYVNDCELVAAIARTDLKKRNDYPLASKDS 240
OY 112 -KTLGCAAVGTREDDKYRLDLLTQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 170
1 -KTLGCAAVGTREDDKYRLDLLTQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 170
Db 241 OKOLLGCAAVGTREDDKYRLDLLTQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 300
OY 171 GGNVVTAAQAOKNLLIDAGVDGLRVGMCGSGICTIQEYVACGRPOGTAVYKAEYARFRGVP 230
1 GGNVVTAAQAOKNLLIDAGVDGLRVGMCGSGICTIQEYVACGRPOGTAVYKAEYARFRGVP 230
Db 301 GGNVVTAAQAOKNLLIDAGVDGLRVGMCGSGICTIQEYVACGRPOGTAVYKAEYARFRGVP 360
OY 231 IADGGIQTGVGHVVKALALAGASTVMMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 290
1 IADGGIQTGVGHVVKALALAGASTVMMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 290
Db 361 IADGGIQTGVGHVVKALALAGASTVMMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 420
OY 291 EKSSSSOKRYFSEBGDKVKIAGVSGSIODKSGIOKFVYLLIAGIQHGCODIGARSLSVLR 350
1 EKSSSSOKRYFSEBGDKVKIAGVSGSIODKSGIOKFVYLLIAGIQHGCODIGARSLSVLR 350
Db 421 EKSSSSOKRYFSEBGDKVKIAGVSGSIODKSGIOKFVYLLIAGIQHGCODIGARSLSVLR 480
OY 351 SMYSGELKFEKRTMSAQIEGVGHLSHYEKRILY 384
```

```
Db 481 SMYSGELKFEKRTMSAQIEGVGHLSHYEKRILY 514

RESULT 2
B31997
IMP dehydrogenase (EC 1.1.1.205) - Chinese hamster
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydroge
C:Species: Cricetus griseus (Chinese hamster)
C>Date: 13-Nov-1998 #sequence_rev1sion 13-Nov-1998 #text_change 05-May-2000
C:Accession: B31997
J:Collart, F.R.; Huberman, E.
R: Biol. Chem. 263, 15769-15772, 1988
A:Title: Cloning and sequence analysis of the human and Chinese hamster inosine-5'-mo
A:Reference number: A92676; MUID:89008491
A:Accession: B31997
A:Molecule type: mRNA
A:Residues: 1-514 <COL>
A:Cross-references: GB:J04209; NID:q19119; PIDN:AAA36993.1; PID:q304517
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal hmo
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHM>
F:117-168/Domain: CBS homology <CBS1>
F:217-232/Domain: CBS homology <CBS2>
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted
```

```
Query Match 84.7%; Score 1655; DB 1; Length 514;
Best Local Similarity 63.6%; Pred. No. 7, 7e-114;
Matches 327; Conservative 31; Mismatches 26; Indels 130; Gaps 1;

OY 1 MADYLSGCGTGYPPEDGTLTAQOLFASADGLTYNDFLTPGFIDEVDTLSALTRKIT 60
1 MADYLSGCGTGYPPEDGTLTAQOLFASADGLTYNDFLTPGFIDEVDTLSALTRKIT 60
Db 1 MADYLSGCGTGYPPEDGTLTAQOLFASADGLTYNDFLTPGFIDEVDTLSALTRKIT 60
OY 61 LKTPLISSPMDVTYTDADMAIAMLAMGIGIFIHNCPTPEOFANEVRKYKFD----- 111
1 LKTPLISSPMDVTYTDADMAIAMLAMGIGIFIHNCPTPEOFANEVRKYKFD----- 111
Db 61 LKTPLISSPMDVTYTDADMAIAMLAMGIGIFIHNCPTPEOFANEVRKYKFD----- 111
OY 112 ----- 111
112 ----- 111
Db 121 LSPKDRVDVFEAKARHGFSGIPITDTGRMGSRVLGISSRDIDFLKEEHRFLIEIMT 180
OY 112 ----- 111
112 ----- 111
Db 181 KREDLVVAAPAGVTLKEANELLORSKKGKLPYVNDCELVAAIARTDLKKRNDYPLASKDA 240
OY 112 -KTLGCAAVGTREDDKYRLDLLTQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 170
1 -KTLGCAAVGTREDDKYRLDLLTQAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 170
Db 241 KROLLGCAAGTHEDDKYRLDLLALAGVDVIVLSSQSGNSVYOIAMVHYIKORYPHLOVY 300
OY 171 GGNVVTAAQAOKNLLIDAGVDGLRVGMCGSGICTIQEYVACGRPOGTAVYKAEYARFRGVP 230
1 GGNVVTAAQAOKNLLIDAGVDGLRVGMCGSGICTIQEYVACGRPOGTAVYKAEYARFRGVP 230
Db 301 GGNVVTAAQAOKNLLIDAGVDGLRVGMCGSGICTIQEYVACGRPOGTAVYKAEYARFRGVP 360
OY 231 IADGGIQTGVGHVVKALALAGASTVMMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 290
1 IADGGIQTGVGHVVKALALAGASTVMMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 290
Db 361 VIADGGIQTGVGHVVKALALAGASTVMMGSLAATTEAPGEFFSDGVRLKKYRGMGSLDM 420
OY 291 EKSSSSOKRYFSEBGDKVKIAGVSGSIODKSGIOKFVYLLIAGIQHGCODIGARSLSVLR 350
1 EKSSSSOKRYFSEBGDKVKIAGVSGSIODKSGIOKFVYLLIAGIQHGCODIGARSLSVLR 350
Db 421 KHLSSONRYFSEADKIKTAQVSGAVODKSGIHKRVPLIAGIQHGCODIGAKSLTOVR 480
OY 351 SMYSGELKFEKRTMSAQIEGVGHLSHYEKRILY 384
1 SMYSGELKFEKRTMSAQIEGVGHLSHYEKRILY 384
Db 481 AMYSGELKFEKRTMSAQIEGVGHLSHYEKRILY 514

RESULT 3
```


Query Match **83.9%**, Score 1640; DB 1; Length 514;

Dd 121 LSPRDVADVDVEAARAHGFCIPITTDGRMSRLVGIISSRDIIDFLKEEBHDFLEIMT 180
Oy 112 ----- 111

Dd 181 KREDIVNPAGITLTKAEANEIILQSRKKGKLPIVNEDDELVAIIARTDKKNRDDPLASKDA 240
Oy 112 -KTLLCGAAAGCTREDDPKRIDLLTGAGDVYVLDSOGNSXYQIAMHHYIKOKYPHLQYT 170
Dd 241 KKQLCGLGAISTHEBDKRIDLDLAQAGDVVVLDSSOGNSTFQINMIRKYTIKDYPNLQVT 300
Oy 171 GGNVNTAAQAANLLIDAGVDSLVRGMGGSGSICITQEVAACGRPHQGTAVYYKAETAYRRGPV 230
Dd 301 GGNVNTAAQAANLLIDAGVDALRVGMGSGSICITQEVLAACGRPQTATAYKKSEVARARRGVP 360
Oy 221 IIA DGGIOTGVGHVKALALGASTVMWGSLLAATTAEAGEVFPSFGVKLRKITRGMSGIDAM 290
Dd 361 VIADGGIONVNHIKALKLGASTVMWSLLAATTAEAGEVFPSFGIRLKRYRGMSGIDAM 420
Oy 291 EKSSSKORRYESEGKVLYTAAGVSGSIDDKSIGKFPPYLLAGIQHGCDIGAKSLTVLR 350
Dd 421 DKHLSSQRNRYSSEADKITYAGVSAGAODKRSIHKFPYPLLAIQHSCDIGAKSLTVLR 480
Oy 351 SMTYSGLKFEKRTIMSQAQIEGVHGLHSYEERLY 384
Dd 481 AMMYSGELKFEKRTISSAQEGVSHLSHYEKRLF 514

RESULT 4

JT0565
IMP dehydrogenase (EC 1.1.1.205) - mouse
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydroge
C:Species: Mus musculus (house mouse)
C>Date: 13-Nov-1998 #sequence.revision 13-Nov-1998 #text_change 05-May-2000
C:Accession: JT0565; A34375; S42724
R:Tiedeman, A.A.; Smith, J.M.
Gene 97, 289-293, 1991
A>Title: Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase.
A:Reference number: JT0565; MUID:91153661
A:Accession: JT0565
A:Molecule type: mRNA
A:Residues: 1-514 <TF>
A:Cross-references: GB:M33934; NID:g198393; PIDN:AAA39311.1; PID:g309413
R:Hodges, S.D.; Pung, E.; McKay, D.J.; Renaux, B.S.; Snyder, F.F.
J.Biol. Chem. 264, 18137-18141, 1989
A>Title: Increased activity, amount, and altered kinetic properties of IMP dehydrogen
A:Reference number: A34375; MUID:90036890
A:Accession: A34375
A:Molecule type: protein
A:Residues: 125-134;182-194;289-290;439-449;456-457,'L',459-464,'S',466;475-478 <ROD>
R:Lightfoot, T.; Snyder, F.F.
Biochim. Biophys. Acta 1217, 156-162, 1994
A>Title: Gene amplification and dual point mutations of mouse IMP dehydrogenase assoc
A:Reference number: S42724; MUID:94153991
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-332,'T',334-350,'Y',352-482,'W',484-514
A:Cross-references: EMBL:M98333; NID:g425157; PIDN:AAA20181.1; PID:g425158
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, November 1993
C:function:
A:description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu
A:pathway: purine nucleotide biosynthesis
C:superfamily: IMP dehydrogenase: CBS homology; IMP dehydrogenase amino-terminal homo
C:keywords: duplication, GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
F:30-96/Domains: IMP dehydrogenase amino-terminal homology <IDHN>
F:117-168/Domains: CBS homology <CBS1>
F:184-232/Domains: CBS homology <CBS2>
F:233-476/Domains: IMP dehydrogenase catalytic homology <IDHC>
F:331/Active site: Cys #status predicted

[illegible]


```

Query Match 53.4%: Score 1238.5; DB 1; Length 523;
Best Local Similarity 48.6%: Pred. No. 2.9e-83;
Matches 244; Conservative 62; Mismatches 63; Indels 133; Gaps 3;

16 DGLTAAQLQLEAS--ADGLTYNDNFLILPGFIDFADEVDLTSALTTRKTLTKPLTSSPMDTV 73
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
21 DGLSVQELMDSTKTRGLTYINDFLVPLGLVDFPSSSEVSLQTKLTKRNTLTTPVSSPMDTV 80
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
74 TEADMAIAMLALMGIGCFIHHNCTPEFQANEVRKVKFD----- 111
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
81 TESEMAIFALLGIGCFIHHNCTPEQADAMVRKVENGFNNPVIPTTVEAKSM 140
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
112 ----- 111
141 KERFGSGFPVTEDEGRNKLMLGIVTSRDIOFEVDNSLLVDVMTRKNPVTGAQGITLSE 200
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
112 ----- KTLGGAAGTRED 126
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
201 NEILKKIKKSKLLIYDDNGLNLSMRDLMKNQVPLASKSATTKQLLGLAIGITIDAD 260
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
127 KYFLDLTQAGVDVIVLDSSQGSNSVYQIAMVHYIKOKYPHLQVIGNVVTAQAANKLIDA 186
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
261 KKRLLRLVLEAGDVLVDSSQGSNSIFQLNMKIMKIKETPEDLFIIGNVATREQAANLIA 320
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
187 GVDGLRVGCGCSICITQGVMAAGRRPGQAVYKVAEYARREVPVPIADGIGDTVGHVYKA 246
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
321 GADGLRLIGSSSICITQGVMAAGRRPGQAVYKVAEYARREVPVPIADGIGDTVGHVYKA 380
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
247 IALGASTVMGSLIATTEAPGEYFSDGVRLKRRKRGMSLDAMERS-----SSQKRFES 302
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
381 IALGSTVVMGMLAGTTESPEYFYQDGKRRLAKAIRGMSIDAMKLTGKKGAAISRRES 440
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
303 EEDKVIKIAQVSGSIQDGSIQKFPVYLIAGIQHCODIGARSLSVLSMYSGLKREK 362
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
441 ESDSVLVAGVSGAVVDGKSIKFFIPLYLNGLQHSODIGYKSTLTKENQSGKRVREF 500
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
363 RTMSAIDGGVGHLSYEKRL 384
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||
501 RTASQLEBGGVHNHLSYEKRL 522
   ||| :|| :||| ||||| ||| :|| :|| :|| ||| ||| ||| ||||| |||

RESULT 9
S48997
IMP dehydrogenase (EC 1.1.1.205) PUR5 - yeast (Saccharomyces cerevisiae)
N:Alternate names: Inosine 5'-monophosphate dehydrogenase (IMPDH); protein YHR216w
C:Species: Saccharomyces cerevisiae
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 23-Mar-2001
C:Accession: S48997
R:Macri, C.
submitted to the EMBL Data Library, February 1994
A:Description: The sequence of S. cerevisiae cosmid 9177.
A:Reference number: S48997
A:Accession: S48997
A:Molecule type: DNA
A:Residues: 1-523 <MAC>
A:Cross-references: EMBL:U00029; NID:9551322; PIDDN:RAAB9728.1; PID:9458916; GSPDB:GND0000
C:Genetics:
A:Gene: PUR5; MIPS:YHR216w
A:Map position: 8R
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:187-235/Domain: CBS homology <CBS>
F:236-464/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:335/Active site: Cys #status predicted

```

QY 16 DGLTAAQLFASADGLTYNDFFLLPGFIDFIADDEVDTLSALTRKTLTKPLTSLSSPMQVTE 73
Best Local Similarity 44.1%, Pred. No. 1,le-72;
Matches 219; Conservative 66; Mismatches 83; Indels 129; Gaps 3;

16 DGLTAAQLFASADGLTYNDFFLLPGFIDFIADDEVDTLSALTRKTLTKPLTSLSSPMQVTE 75

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Db 13 DGTAAEELF--SQDGLSFNDFITLPGFIDFSSKYNVSGQFTKNILHLPLVSSPDVTE 71
QY 76 ADMATAMLMGCGIGFIHNCPEFOANVRKYKKE----- 110
Db 72 SSMARAAALMGIGIYIHNCIVEODARVRYSVKLYRNGFIKPKSVSPDYVSTIRNKS 131
QY 111 -----DKT-----LLCGAAGTREDDK 127
Db 132 EKGISGLVTEGGKYDKGLIGVCTKIDFVKDASAPVSQYMTRENNMTVERYPKLEEA 191
QY 111 -----DKT-----LLCGAAGTREDDK 127
Db 192 MDVILNRSRHYLPVLNDEDEVVCLSRDPAVARADYPNSSLDNRNHLCAATSTREDDK 251
QY 128 YRLDILTOAGVDYIVLDDSSQNSVYQIAMVHYIKOKYRPHLOVIGSNVYTAQAOKNLIDAG 187
Db 252 GRVAALSEAGIDVVLDDSSQNTIYQVSFIRWKKTPYHLEVVAGNVVTOQAOKNLIDAG 311
QY 188 VDLGRVWGCGSICITQEVNACGRPOGTAVYKVAEYARRFVPIADGIGTGVHVKAL 247
Db 312 ADSLRIGMGSSICITQEVNACGRPOGTAVYKVAEYARRFVPIADGIGTGVHVKAL 371
QY 248 ALGASTVMGSLAATTEAPGEYFFSDGVRLKRYRGMSLDAMEKSSSSOKRYFSEGDYV 307
Db 372 AVGANVAMLGSMIACTSETPEYFFKDGMRLLKRYRGMSLDAMEKSSSSOKRYFSENEETL 431
QY 308 KIAQGVSSIQDKGSIQKFPYLLAGIQHGCODIGARSLSVLSMMYSGELKFEKRTMSA 367
Db 432 QVAGGVAGVLDKGSVLLKLAIVYHKGLOQSAODIGESFDAIREKVEGYLENNRTLLTA 491
QY 368 QIEGCVHGLHSYERKLY 384
Db 492 QSEGAVSHLHYERKLF 508

RESULT 11
A38668
IMP dehydrogenase (EC 1.1.1.205) - Leishmania donovani
N:Alternate names: IMPDH; Inosine 5'-monophosphate dehydrogenase
C:Species: Leishmania donovani
C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 16-Jul-1999
C:Accession: A38668
R:Wilson, K.; Collart, F.R.; Huberman, E.; Stringer, J.R.; Ullman, B.
J. Biol. Chem. 266, 1665-1671, 1991
A:Title: Amplification and molecular cloning of the IMP dehydrogenase gene of Leishmania
A:Reference number: A38668; MUID:91107664
A:Accession: A38668
A:Molecule type: DNA
A:Residues: 1-514 <MID>
A:Cross-references: GB:M55667; NID:g159360
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:179-94/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:179-228/Domain: CBS homology <CBS>
F:229-472/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:327/Active site: Cys #status predicted

```

```

Query Match 55.6%; Score 1087.5; DB 1; Length 514;
Best Local Similarity 43.8%; Pred No. 3.5e-72;
Matches 218; Conservative 62; Mismatches 89; Indels 129; Gaps 3;

QY 15 EDGLTAQQLFASADGLTYNDPLILPGFIDFIADVDLSALTRKILTKPLISSPDVYT 74
Db 14 KKGCAAEELF--RGDGLTYNDFTILPGFIDFGAADVNISQFTKRLRLHPYVSSPDVIT 72
QY 75 EADMAIALMAGCGIGFIHNCIPEFOANVRKYKKE----- 110
Db 73 ENEMAKTAMLMGIVGLHNCIPEFOANVRKYKAVRNGFISKPKSVSPNPPTISNIRIK 132

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QY 111 -----DKT-----LLCGAAGTREDDK 126
Db 133 EKGISGLVTEGGKYDKGLIGVCTKIDVYKKKDPVSAVMTRENNMTVERAPIDLEE 192
QY 111 -----DKT-----LLCGAAGTREDDK 126
Db 193 AMDVILNRSRYLPVLNDEDEVNMLCSRDAVARADYPHSTLDKSGRLICAAATSTRED 252
QY 127 KYRDLTOAGVDYIVLDDSSQNSVYQIAMVHYIKOKYRPHLOVIGSNVYTAQAOKNLIDA 186
Db 253 KRVVAALADGVVDVVLDDSSQNTIYQIAFTKWKSTYHLEVVAGNVVTOQAOKNLIDA 312
QY 187 GVDGLRWGCGSICITQEVNACGRPOGTAVYKVAEYARRFVPIADGIGTGVHVKVA 246
Db 313 EADGIRIGMGSSICITQEVNACGRPOGTAVYKVAEYARRFVPIADGIGTGVHVKVA 372
QY 247 LALGASTVMGSLAATTEAPGEYFFSDGVRLKRYRGMSLDAMEKSSSSOKRYFSEGDY 306
Db 373 LAIGANCMGLMGLSGTETPEYFFKGVRLKYRGMGSLDAMEKSSSSOKRYFSENEEA 432
QY 307 VKIAQGVSSIQDKGSIQKFPYLLAGIQHGCODIGARSLSVLSMMYSGELKFEKRTMS 366
Db 433 QVAGGVAGVLDKGSVLLKLAIVYHKGLOQSAODIGESFDAIREKMYAGVLENNRSP 492
QY 367 AOIEGCVHGLHSYERKLY 384
Db 493 AQEGGVSHLSYERKLF 510

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RESULT 12
T40127
IMP dehydrogenase (EC 1.1.1.205) SPBC2F12.14c - fission yeast (Schizosaccharomyces po
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; Inosine 5'-monophosphate dehydroge
C:Species: Schizosaccharomyces pombe
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jul-2000
C:Accession: T40127; T42083
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, June 1997
A:Reference number: Z21907
A:Accession: T40127
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-524 <MID>
A:Cross-references: EMBL:T42083; PIDN:CA810161.1; GSPDB:GM00067; SPDB:SPBC2F12.14c
A:Experimental source: strain 972b; cosmid c2F12
R:Yoshioaka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722
A:Accession: T42083
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 62-252; 'G', 254-262, 'P', 264-293 <YOS>
A:Cross-references: EMBL:D89106; NID:g1749419; PIDN:BA13769.1; PID:g1749420
A:Experimental source: strain PR745
C:Genetics:
A:Gene: SPDB:SPBC2F12.14c
A:Map position: 2
A:Introns: 153/1
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:124-174/Domain: CBS homology <CBS1>
F:187-237/Domain: CBS homology <CBS2>
F:238-486/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:337/Active site: Cys #status predicted

```

```

Query Match 55.1%; Score 1076.5; DB 1; Length 524;

```

Best Local Similarity 44.18%; Pred. No. 2,3e-71;
Matches 224; Conservative 58; Mismatches 91; Indels 135; Gaps 3;

```

Oy 12 YPEEDGLTAQOOLFAS--ADGLTYNDPLILPGFIDFIADVDLTSLTKRITLKPLISSP 69
    ||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 17 YEKKGSLIDDLIRNFGGGLFNFDFLLPGIDFVPNNVSLERTISNITVLTKEPFSMP 76
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 70 MDVTEDAMATMALMGIGFIHNCPTPEQANEVRYKKFD----- 111
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 77 MDVTEDAMATMALMGIGFIHNCPTPEQANEVRYKKFD----- 111
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 112 ----- 111
Db 137 VLKIKETGFGSIPITENGKLGKLVGIVTSRDVOFHKDTMPTVEVMTPEELITTAEG 196
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 112 -----KTLGCAAV 120
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 197 ISLERANEMLRKKKGLPVDKDONLVALSLTDLMKNLHPLASKTSQDKQLMVAAI 256
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 121 GTREDDKRLDLTOAGVDVIVLDSOGNSVYQIAMVHYTKQYPHLOVIGGNVTAQA 180
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 257 GTRDDRLRLALAEAGIDAVVIDSQNSCFQIEMIKIKTPKIDVINGNVVTTREOT 316
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 181 KNLIDAGVDGLRVGKSGSICITQEVMAGRPGGTAVYKAEYARREGVPIIADGIGIOTV 240
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 317 ASLIAAGADGLRVGKSGSACITQEVMAGRPGGTAVYKAEYARREGVPIIADGIGIOTV 376
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 241 GHVYKALALGASTYMGSLAATTEAPGEYFSDGRLKRYKRGSLDAME-----KSSSS 296
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 377 GHVYKSLSGATAVVMGGLTAGTTEPGEYVREGORAKSYRGMGSTIAMGCTGKNNAS 436
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 297 OKRYSSEDDKXKIAOGVSGSIQDKSGIOKEFVYPIIAGIQHCODIGARSLSLRSMYSG 356
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 437 TGRFSEDDAVVAVVQVSGSLVVDKSLRFLPYLTGTGLHALODIGTKSLDELHVAADKH 496
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 357 ELKPEKFTMSAOIEGGVGHLSHYEKRLY 384
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 497 EVREFELNSSAIRREGDIOGFATYERKLT 524
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 13

T32709
IMP dehydrogenase (EC 1.1.1.205) T22D1.3 - *Caenorhabditis elegans*
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; Inosine-5'-monophosphate dehydrogenase
C:Species: *Caenorhabditis elegans*
C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
R:Accession: T32709
R:Submitted to the EMBL Data Library, December 1997
A:Description: The sequence of *C. elegans* cosmid T22D1.
A:Reference number: Z21211
A:Accession: T32709
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-499 <GBI>
A:Cross-references: EMBL:AF039052; PDB:AA94282.1; GSPDB:GN00022; CESP:T22D1.3
A:Experimental source: strain Bristol N2; clone T22D1
C:Genetics:
A:Gene: CESP:T22D1.3
A:Map position: 4
A:Insertions: 35/2; 85/3; 159/1; 183/3; 342/1; 412/3; 493/2
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
F:120-170/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:188-238/Domain: CBS homology <CBS1>
F:239-461/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:337/Active site: Cys #status predicted

Query Match 53.2%; Score 1039.5; DB 1; Length 499;
Best Local Similarity 43.9%; Pred. No. 1.1e-68;
Matches 221; Conservative 55; Mismatches 72; Indels 155; Gaps 5;

```

Oy 16 DGLTAQOLFASAGCTYNDPLILPGFIDFIADVDLTSLTKRITLKPLISSPMTYRE 75
    ||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 18 DGETVHBMMAHKAAGLYNDPLILPGFIDFVNHVSLSETNITKDLKAPLVSSPMOTYRE 77
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 76 ADMAIAMAALMGIGFIHNC--TPEQANEVRYKKF-----DKT----- 113
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 78 SGMAIYVALGIGIIGHNCPKPEDQAEVLKRYKRGVYVMPHCLSRSTAFMIQIK 137
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 114 ----- 113
Db 138 KKYGTGAPYTEDGVRGSKLIGHVTSRDFEITMDVAGOKGTPISDINVSVDQLHGHIN 197
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 114 -----LLGCAAV 121
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 198 DAPLSOKLKEHRLGLPVDNDELCLALCSDLKARDYPMASYDSKQLLCAAVN 257
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 122 TREDDKRLDLTOAGVDVIVLDSOGNSVYQIAMVHYTKQYPHLOVIGGNVTAQAQ 181
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 258 TGRSGYTVADVAYEAGVDVIVLDSOGNSVYQIAMVHYTKQYPHLOVIGGNVTAQAQ 317
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 182 NLDAGVDGLRVGKSGSICITQEVMAGRPGGTAVYKAEYARREGVPIIADGIGIOTV 241
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 318 LLIDOGADGLRIGMGSGSICITQEVMAGRPGGTAVYKAEYARREGVPIIADGIGIOTV 377
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 242 HVYKALALGASTYMGSLAATTEAPGEYFSDGRLKRYKRGSLDAMEKSSSGKRYE 301
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 378 YITKALSLGASAVVMGGLTAGTTEAPGEYFSDGRLKRYKRGSLDAMEKSSSGKRYE 416
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 302 SESDKYKIAOGVSGSIQDKSGIOKEFVYPIIAGIQHCODIGARSLSLRSMYSGELKEP 361
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 417 SESDQIKVAGVSATKMDKSGCHKFLPYLRGQHMODIGVRSULDFEKKDNGLVKRE 476
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Oy 362 KRTMSAOIEGGVGHLSHYEKRLY 384
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 477 RRTSNAQIEGGVGHLSHYEKRLY 499
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 14

F86298
IMP dehydrogenase (EC 1.1.1.205) - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C:Accession: F86298
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Malt, R.; Marzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: AB6141; MUID:21016719
A:Accession: F86298
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <STO>
A:Cross-references: GB:AE005172; NID:g4966356; PDB:RAD34687.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Keywords: GMP biosynthesis; NAD; oxidoreductase

Query Match 52.0%; Score 1016; DB 2; Length 502;
Best Local Similarity 42.0%; Pred. No. 6e-67;
Matches 210; Conservative 61; Mismatches 97; Indels 132; Gaps 2;
Oy 15 EDGLTAQOLFASADGLTYNDPLILPGFIDFIADVDLTSLTKRITLKPLISSPMTYVT 74

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Db      5 EDGFEAEKLFSGYASYTDVYILPHFIDFSDAVSLSTRLSKRPVLSIPCAVSMPTDVS 64
      75 EADMAIAMAALMGIGIFHINCTPPEQANEVRKKVF----- 110
Db      65 ESHMAAAMAALGGIGIVHNCIDIDIDQASVIRHAKSLQVPIASDAVFKCPHQIGSVDDFG 124
      111 ----- 110
Db      125 PSSFEVFSQGTGLLPKLLGIYVSKSEWSSMKDDQKEVKIYDMKSCENKDYIYVPMIDIDK 184
      111 -----DKTLGGAAGTIRE 124
Db      185 IEAVLEDKQKGFVLEKEGEFVNVYTKDVERVKYPRKLGSGTGAADKKMVGALIGIRE 244
      125 DDKTRLDLLTQAGVDVYILDSQGSNYYQIAMVHYIKOKYPHLOVIGGNVYTAQAQNL 184
      245 SDKERLEHLVAGANVAVVLDSSQGSNIYOLEMIKYKNTYBELDVAGNVYTMQAEML 304
      185 DAGVGLRVGSGGICITQEVMAAGRPQGTAVYKVAEYARFRGPIIADGGIQTGVH 244
      305 KAGVDGLRVGSGGICITQEVCAVGRQATVYKSTLAQHGVPVADGGISNSGHI 364
      245 KALALGASTVMGSLLAATTEAPGEYFSDGYRLKRYGMSLIDAMEKSSSQKRYFSG 304
      365 KALYLGASTVMGSLFLAGSTEAPGAYEYRNGRVRKRYGMSLEAMTK--GSDQRYLGD 422
      305 DKVRIAGVSGSIDQKSIQKFPYLLAGIQHCCODIGARSLSVLRSMYSGELFEKRT 364
      423 AKLKIAGVGVAGVADKGSVLKFIPTMHAHVKGQFDLGASLSQSAHELLRDLNTLRLEART 482
      365 MSAQIEGVGHLSYERKRLY 384
      483 GAAQIEGVIHGLVSYERKSF 502

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RESULT 15

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JG4999
IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JG4999
R:Collart, F.R.; Osipuk, J.; Trent, J.; Olsen, G.J.; Huberman, E.
Gene 174, 217-220, 1996
A:Title: Cloning and characterization of the gene encoding IMP dehydrogenase from Arabidopsis
A:Reference number: JG4999; MUID:97045815
A:Accession: JG4999
A:Molecule type: DNA
A:Residues: 1-503 <COL>
A:Cross-references: GB:L34684; NID:g1100062; PIDN:AB41940.1; PID:g1100063
C:Genetics:
A:Gene: Impdh
A:Introns: 135/1; 334/3; 404/3; 490/3
C:Complex: homotetramer
C:Function:
A:Description: provides precursors for DNA and RNA biosynthesis; it catalyzes the conversion of IMP to XMP
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
C:Keywords: GMP biosynthesis; NMD; oxidoreductase; purine nucleotide biosynthesis
F:20-86/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:172-220/Domain: CBS homology <CBS2>
F:221-465/Domain: IMP dehydrogenase catalytic homology <IMP>
F:322/Active site: Cys #status predicted

```

Query Match 51.5%; Score 1007.5; DB 1; Length 503;

Best Local Similarity 42.1%; Pred. No. 2.5e-66;

Matches 211; Conservative 62; Mismatches 95; Indels 133; Gaps 4;

15 EDGLTAQOLFASADGLTNDPLIPGFIIDFIDEVDLTSALRKTITKPLISSPMPTV 74

5 EDGFPADKLFAGGYSTYTDVILPHFIDFSDAVSLSTRLSKRPVLSIPCAVSMPTDVS 64

75 EADMAIAMAALMGIGIFHINCTPPEQANEVRKKVF-----TPPEQ 100

```

Db      65 ESHMAAAMAALGGIGIVHNCIAGQASTIRQAKSLKHPIASDAGVRKPEYEITSLDAFG 124
      101 ----- 100
      125 PSSFEVFSQGTGLLPKLLGIYVSKSEWSSMKDDQKEVKIYDMKSCENKDYIYVPMIDIDK 184
      101 -----ANEVRKRYKFEKRT-----LLCGAAGTIR 123
      185 KLEFVLEDKQKGFVLEKEGEFVNVYTKDVERVKYPRKLGSGTGAADKKMVGALIGIRE 244
      124 EDDKTRLDLLTQAGVDVYILDSQGSNYYQIAMVHYIKOKYPHLOVIGGNVYTAQAQNL 183
      245 ESDKERLEHLVAGANVAVVLDSSQGSNIYOLEMIKYKNTYBELDVAGNVYTMQAEML 304
      184 IDAGVDGLRVGSGGICITQEVMAAGRPQGTAVYKVAEYARFRGPIIADGGIQTGVH 243
      305 IAGVDGLRVGSGGICITQEVCAVGRQATVYKSTLAQHGVPVADGGISNSGHI 364
      244 VKALALGASTVMGSLLAATTEAPGEYFSDGYRLKRYGMSLIDAMEKSSSQKRYFSG 303
      365 KALYLGASTVMGSLFLAGSTEAPGAYEYRNGRVRKRYGMSLEAMTK--GSDQRYLGD 422
      304 GPKVRIAGVSGSIDQKSIQKFPYLLAGIQHCCODIGARSLSVLRSMYSGELFEKRT 363
      423 QTKLKIAGVGVAGVADKGSVLKFIPTMHAHVKGQFDLGASLSQSAHELLRDLNTLRLEART 482
      364 TMSAQIEGVGHLSYERKRLY 384
      483 TGAQIEGVIHGLVSYERKSF 503

```

RESULT 16

```

S53477
IMP dehydrogenase (EC 1.1.1.205) FUN63 - yeast (Saccharomyces cerevisiae)
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein YAR073w
C:Species: Saccharomyces cerevisiae
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: S53477
R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Ka
submitted to the EMBL Data Library, February 1994
A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of th
A:Reference number: S53458
A:Accession: S53477
A:Molecule type: DNA
A:Residues: 1-403 <BUS>
A:Cross-references: EMBL:L28920; NID:g1616966; PIDN:AAC09509.1; PID:g456156; GSPDB:GN
C:Genetics:
A:Gene: FUN63; MIPS:YAR073w
A:Map position: 1R
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: GMP biosynthesis; NMD; oxidoreductase; purine nucleotide biosynthesis
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:187-235/Domain: CBS homology <CBS>
F:236-403/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:335/Active site: Cys #status predicted

```

Query Match 35.4%; Score 691.5; DB 1; Length 403;

Best Local Similarity 41.2%; Pred. No. 3e-43;

Matches 145; Conservative 35; Mismatches 43; Indels 129; Gaps 2;

16 DGLTAQOLFAS--ADGLYNDPLIPGFIIDFIDEVDLTSALRKTITKPLISSPMPTV 73

21 DGLSVQELMDSKIRGSLAVNDELIPGLVDFASSFSQTKLRLNTLNIPIVSSPMPTV 80

74 TEADMAIAMAALMGIGIFHINCTPPEQANEVRKKVF----- 111

81 TESEMATFMAALDGGIGIFHINCTPPEQADMDVRRVKNYENGFINNPVISPPTTGEANSK 140

QY 112 ----- 111
Db 141 KEKYGAGFPVADGKRNALVGAITSRDIQFVEDNSLVQDVMTKNPVTGAQGITLSEG 200
QY 112 -----KTLGCAAVGTREDD 126
Db 201 NEILAKIKKGRRLVYDEKGNLYMSLSTDLKMNKYPLASKSANTKOLLMGASIGTMDAD 260
QY 127 KYRLDLTQAGVDVIVLSSQGSNVSQYIAVHYIKOKYPHLOVIGNVVTAQAQKNLIDA 186
Db 261 KERRLILVAGLVDVILSSQGSNIFQNLNMIKIKETFPDLLETAGNVVTKQGANLIIAA 320
QY 187 GVGCLRVGMCSCICTQEVYACGRPGGTAVYKAEYARFRVPIIDGCIQ 238
Db 321 GAGBLRIGMGTSICITQKWKACGRPGGTAVYVCEANOFVGCMAADGGVQ 372

RESULT 17
D97232
IMP dehydrogenase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: D97232
R:Rolling, J.; Breton, G.; Omselchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum* ATCC824
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: D97232
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-485 <RUR>
A:Cross-references: GB:AE001437; PIDN:AAK80647.1; PID:g15025734; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2701
C:superfamily: IMP dehydrogenase: CBS homology; IMP dehydrogenase amino-terminal homolog

Query Match 34.5%; Score 674; DB 2; Length 485;
Best Local Similarity 35.4%; Pred. No. 7.3e-42;
Matches 168; Conservative 52; Mismatches 118; Indels 136; Gaps 4;

QY 31 TYNDFLLPGEFIDFIADVDLTSAITRKITPLISSPMDVTADMAIAMLGSGIF 90
Db 10 TFDVGLVLPKSEVLPKEVDLTNLTKIKINIPILMSAGMDVTSKMAIAMAREGIGI 69
QY 91 IHNNCTPEFOANEVRYKKF----- 108
Db 70 IHNNMTAEQASEVDKVRKQENGVTNPISLSKDNSVOEALDLMKRIRISGVPIITDNACK 129
QY 109 -----KFDK----- 112
Db 130 LIGLITNRDIFENDYSKRIEELMTTENTLTAPOGTTIDEAKNLLKKHKEKPLVDENF 189
QY 113 -----TLGCAVGTREDDKYRLDLTQAGVDVIVLSS 146
Db 190 VLKGLITIKDIKIRKFPNNAKDSQGLICGAGVGTAKMMDRVKALVDAVSIVVILDTA 249
QY 147 QGNSVYQIAVHYIKOKYPHLOVIGNVVTAQAQKNLIDAGVDGLRVGMCSCICTQEV 206
Db 250 HGSQGVLEAVKTKKAYPELOVIAAGNVATAAVALHDLIEGADVGVIGPSICTTRV 309
QY 207 MACGRPGTAVYKAEYARFRVPIIDGCIQTVGHVVKALAGASTVMGSLAATTEA 266
Db 310 AGIGVQQLAVAMCVBEANKYVPIITADGIRKSCDILVAKALAGAAVAMGSMFACCEA 369
QY 267 PGEYFSDGVRLKRYKMGSLDAMEKSSSQKRYFSEGDVKVIAQVSGSIDQKGIQK 326
Db 370 PGEYFSDGVRLKRYKMGSLDAMEKSSSQKRYFSEGDVKVIAQVSGSIDQKGIQK 326
QY 327 VPIYINGIQHGCDIGARSLVLRSMYSGELKFEKRTMSAQLEGVHGHLSYE 380

Db 428 VFOILGIRSGMGYILSRNMTL-----FEKATFVQTSAGLRSHPHD 471

RESULT 18
G81308
IMP dehydrogenase (EC 1.1.1.205) Cj1058c [similarity] - Campylobacter jejuni (strain N/Altenate names: IMP-NAD+ oxidoreductase; IMPDH; inosine 5'-monophosphate dehydroge
C:Species: Campylobacter jejuni
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
C:Accession: G81308
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kellley, J.M.; Churcher, C.; Basham, D.; Chl
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals
A:Reference number: A81250; MUID:20150912
A:Accession: G81308
A:Molecule type: DNA
A:Residues: 1-485 <PAR>
A:Cross-references: GB:AL139077; GB:AL111168; MID:g6968444; PIDN:CAB73314.1; PID:g696
A:Experimental source: serotype O2, strain NCYC 11168
C:Genetics:
A:Gene: quab; Cj1058c
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
F:8-74/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:95-143/Domain: CBS homology <CBS1>
F:156-204/Domain: CBS homology <CBS2>
F:205-446/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:301/Active site: Cys #status predicted

Query Match 33.5%; Score 654.5; DB 1; Length 485;
Best Local Similarity 34.5%; Pred. No. 2e-40;
Matches 165; Conservative 57; Mismatches 107; Indels 149; Gaps 8;

QY 30 LRYNDFLLPGEFIDFIADVDLTSAITRKITPLISSPMDVTADMAIAMLGSGIF 89
Db 8 LRFEDVLRGYSSEVLPKEVKIHTKLTNLTMLPILSAMDPVTBHRALIMARIGIGI 67
QY 90 FIHNNCTPEFOANEVRYKKF-----DK 112
Db 68 VIKHNDIASQVEVRYKKSSEGVIIIDPIVSPKASVALEIMAERYISGVVYDEDK 127
QY 113 TLL----- 115
Db 128 KLIGLITNRDLRFESDFSNLVENVMTKMLITAPKCTITDDAEKIRSTKKEKPLVDEQ 187
QY 116 -----CGAAGTREDDKYRLDLTQAGVDVIVLSS 145
Db 188 GRLEGITIKDLKREKPEYDANKDNFRLVGAALVGOMD--RVDALEAGADVIVLSS 245
QY 146 SQGNSVYQIAVHYIKOKYPHLOVIGNVVTAQAQKNLIDAGVDGLRVGMCSCICTQEV 205
Db 246 AHGHSGLIITDYKAIKAKYPNLDLITAGNITATAAALALCAGADAKVIGIGSICITTRI 305
QY 206 VMAAGRGPGTAVYKAEYARFRVPIIDGCIQTVGHVVKALAGASTVMGSLAATTE 265
Db 306 VSGVGVPIQSAIDECVEEANKRGVPIIADGIRKISDIDAKALAVGASSMTISLAGTDE 365
QY 266 APGEYFSDGVRLKRYKMGSLDAMEKSSSQKRYFSEGDVKVIAQVSGSIDQKGS 322
Db 366 SPGEIPTYQISALDECEVEANKRGVPIIADGIRKISDIDAKALAVGASSMTISLAGTDE 422
QY 323 IQKFPYLLIAGIQHGCDIGARSLVLRSMYSGELKFEKRTMSAQI-----EGVH 374
Db 423 IRSVVHQLGLGRSSMGVYGARDIE-----DFOKRAEFELITAGLKESHVH 469

RESULT 19
H70473

C:Genetics:
A:Gene: TM1347
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
C:Keywords: GMP biosynthesis; NAD; oxidoreductase
E:5-71/Domain: IMP dehydrogenase amino-terminal homolog <IDIN>
E:154-202/Domain: CBS homology <CBS>
F:203-444/Domain: IMP dehydrogenase catalytic homology <IDC>
F:301/Active site: Cys #status predicted

Query Match 32.8%; Score 641.5; DB 2; Length 482;
Best Local Similarity 32.8%; Pred. No. 1.8e-39;
Matches 157; Conservative 61; Mismatches 123; Indels 137; Gaps 4;

Qy 28 DGLTYNDPLIPGFDIDAEVDLTALTRKTLTKPLTISSPMPTVEADMAIMAMMG 87
Db 3 EALFFDDLVLPQYSEVLPKDKYIDTRTRQIRINIPLYSAAMPTVEALAKALAREGG 62
Qy 88 IGFHHNCTPPEQANEVRKVK----- 109
Db 63 IGIHKNLTPEQARQYIVKKTENGIIYDPIYTPDKTVEALIDMAEYKIGLPPVDE 122
Qy 110 -----FDKT----- 113
Db 123 EGRVLGLTNDVREKMLSKIKDMLTPREKLLVAPPDLSLEAKETLHQRLEKPLV 182
Qy 114 -----LDCAAVGTREDDKYRLDLTLQAGVDVY 142
Db 183 SKDNKLVGLTIDKIMSYIEHPNARDEKRLVGAAGVSTPELMENEREKLVKAGVDVY 242
Qy 143 LDSSQGSNVYQIAMVHYIKQYIPHLQYIGVNVTAQAQKNLIDAGVDGLRVGCGSIC 202
Db 243 IDTAHGHRRVETLEMKADYDPLPVAGNVATPEGEALIKAGADAVKGVPGSIC 302
Qy 203 TOEWACGRPGDTAVYKAEYARRRGPYIADGGIQYVGHVKKALALGASTVMGSLAA 262
Db 303 TRVAVAGVLPOLTAVMESSEVARKYDPIIADGIRISGDIYKALAGAEVVMGSIIFAG 362
Qy 263 TTEAPGEYFFSDGVRLKRYRGMGLDAMEKSSSQKRYFSEGDYKIAQVSGSIOQGS 322
Db 363 TEEAPGETILYQGRKRYKAYRGMGLGAMR--SGSADRYGQGEKFPVEGIEGVAPKGT 420
Qy 323 IQKVPYLIQIHGCGQDIGARSLSVLRSMYSGELKFEKRTMAQIEGVYHGHSE 380
Db 421 VKDVHOLVGLRSGMGYIGARTKEID-----EKAIVFKITPAGVKESHPHD 468

RESULT 22
H83173
IMP dehydrogenase (EC 1.1.1.205) PA3770 [similarity] - Pseudomonas aeruginosa (strain PA

C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83173
A:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuoguchi, S.D.; Warren, P.; Hickey, M.J.; Bladman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, N.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: H83173
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-489 <STO>
A:Cross-references: GB:AE004796; GB:AE004091; NID:99949939; PIDN:AA607157.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: guaB; PA3770
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog
C:Keywords: GMP biosynthesis; NAD; oxidoreductase

Query Match 32.3%; Score 632; DB 2; Length 489;
Best Local Similarity 33.4%; Pred. No. 8.9e-39;

Matches 159; Conservative 55; Mismatches 130; Indels 132; Gaps 4;

Qy 26 SACLTYNDPLIPGFDIDAEVDLTALTRKTLTKPLTISSPMPTVEADMAIMAMMG 85
Db 5 SQELTDDVLLIPGSEVLPKDKYIDTRTRQIRINIPLYSAAMPTVEALAKALAREGG 64
Qy 86 GIGFIHNNCTPPEQANEVRKVKFD----- 111
Db 65 GIGFIHNNCTPPEQANEVRKVKHETAIYRDPVYTPSTKIELLOMAREYGSFPPV 124
Qy 112 ----- 111
Db 125 EGEELVGIYTRDLRVKPNAGTVAAIMPRDKLVTAARECTPLEEKAKLYENRIEMULV 184
Qy 112 -----KT-----LDCAAVGTREDDKYRLDLTLQAGVDVY 141
Db 185 VDENVYLRGLVTRDIEKATYTPLASDEQGRVLRGAAGVGTADGERVAALVAAAGVDV 244
Qy 142 VLDSSQGSNVYQIAMVHYIKQYIPHLQYIGVNVTAQAQKNLIDAGVDGLRVGCGSIC 201
Db 245 VVDTAHGHSGVIERVWVKOTPPDYVIGGINATAEAAKALAEAGADAVKGVIGPSIC 304
Qy 202 ITQEWACGRPGDTAVYKAEYARRRGPYIADGGIQYVGHVKKALALGASTVMGSLAA 261
Db 305 TRVAVAGVLPOLTAIVNAAALEGTGVPDIIADGGIRFSGLAKAVAGAYCYVMGSMFA 364
Qy 262 ATTEAPGEYFFSDGVRLKRYRGMGLDAMEKSSSQKRYF--SEGDYKIAQVSGSIO 318
Db 365 GTTEAPGEIELFPGGRVSKYRGMGLDAMEKSSSQKRYF--SEGDYKIAQVSGSIO 424
Qy 319 DKSSIQKVPYLIQIHGCGQDIGARSLSVLRSMYSGELKFEKRTMAQIEGVYHGHSE 374
Db 425 YKGLASVIAHOLMGGLRAAGYTGSDIQQMFT-----POFVRIYAGMAESHVH 475

RESULT 23

H82558
IMP dehydrogenase (EC 1.1.1.205) XF2430 [similarity] - Xylella fastidiosa (strain 9a5

C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 03-Aug-2001
C:Accession: B82558
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below

A:Accession: B82558
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-485 <SIM>
A:Cross-references: GB:AE004052; GB:AE003849; NID:9107617; PIDN:AA85229.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briónes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrero, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Porri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmitieri,
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sava
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovsky-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF2430
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: GMP biosynthesis; NAD; oxidoreductase
F:304/Active site: Cys #status predicted

A:Experimental source: strain 168

C:Genetics:

A:Gene: gnaB

C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of

C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homolog

C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

F:11-77/Domain: IMP dehydrogenase amino-terminal homology <IDHN>

F:98-148/Domain: CBS homology <CBS1>

F:161-209/Domain: CBS homology <CBS2>

F:210-451/Domain: IMP dehydrogenase catalytic homology <IDHC>

F:308/Active site: Cys #status predicted

Query Match 32.0%; Score 626.5; DB 1; Length 488;

Best Local Similarity 32.6%; Pred. No. 2.3e-38;

Matches 155; Conservative 61; Mismatches 126; Indels 133; Gaps 3;

Db 26 SAGSLVNDLFLILPGFIDFADEVLTSAITRKITLPLISSPMDVTVEADMAIAMA 85

Db 7 SKEGLTFDDVLLVPAKSEVLPDVLSELTCLKLNIPVISAGMDVTYESAMAIAMARQ 66

Qy 86 GGIGFIHHNCTPEFOANEVRKVKFDK----- 112

Db 67 GGLGIHKMMSIEQOAEQVDKRSERGVITNPFLPDPHQVFAEHLMGKRYRISGVPIV 126

Qy 113 ----- 112

Db 127 NNEEDQKLVGIIITNRDLRFISDSYMSKISDVTKRELVTAASVGTLLDEAEKILQKHIEKL 186

Qy 113 -----TLGGAAGTREDDKYRLDLITQAGVD 139

Db 187 PLVDDQNKLGILITKIDIEKVEIPNSSKDIHGRLIVGAAGVGTDMTRVKKLVEANVD 246

Qy 140 VIVDSOGNSVYQIAVHYIKOKYPHLOYIGNVVTAQAQKNLIDAGVGLRYGMGCGS 199

Db 247 VIVDTAHGHSQVLTNTVTIKIRETYPELNTIAGNVATAEATRALILEAGADVYKVGIPGS 306

Qy 200 ICTQEVNACGRPGGTAVYKVAEYARRRGPILIADGGIQTGVHVKALALGASTVMNGSL 259

Db 307 ICTRVVAGVGPQITAIYDCATEARKHKTIIADGGIKFSGDITKALAGSHAVMLGSL 366

Qy 260 LAATEAPGEYFFSDGYRLKKRYRGMGLDAMEKSSSQKRYFSGDKVYKIAQVSGSIOD 319

Db 367 LAGTSESPGEETIYQGRFRFVYRGMGSVAAMEK--GSKDRYFOENKKFYPEGIEGRTPY 424

Qy 320 KGSIOKFPYLIAGIOHGCODIGARSLSVLRSMYSGELKFEKRTMSAQIEGCVH 374

Db 425 KGPVEETVYQLVGLRSGMGYCGSKDLRALRE-----EAQFIRMTGAGLRSHPH 474

Search completed: September 26, 2002, 08:27:38
Job time: 127 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 26, 2002, 08:26:01 ; Search time 28.36 Seconds
(without alignments)
2342.385 Million cell updates/sec

Title: US-09-853-918-30
Perfect score: 1955
Sequence: 1 MADYIISGTYVPEDGLTA.....MSAQIEGGVHGLHSEYKRLY 384

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SPTREMBL19:**

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	1740.5	89.0	489	4	Q96NU2	Q96nu2 homo sapien
2	1646	84.2	514	11	Q91Z11	Q91z11 mus musculus
3	1323	67.7	445	11	Q9DC16	Q9dc16 mus musculus
4	1198.5	61.3	521	3	Q9P8J2	Q9p8j2 candida alb
5	1144	58.5	529	3	Q9UVL0	Q9uvl0 pneumocysti
6	1076.5	55.1	524	3	O14344	O14344 schizosacch
7	1039.5	53.2	499	5	O9GZB3	O9gzb3 caenorhabdi
8	1016	52.0	502	10	Q9ZPA0	Q9zpa0 glycine max
9	984	50.3	501	10	Q9AY75	Q9ay75 oryza sativ
10	858.5	43.9	510	5	O96387	O96387 plasmodium
11	795	40.7	392	10	Q944T1	Q944t1 glycine max
12	674	34.5	485	16	Q97FM8	Q97fm8 clostridium
13	654.5	33.5	485	16	O9PNN3	O9pnn3 campylobact
14	649	33.2	509	2	Q9RHG9	Q9rhg9 bacillus ce
15	643.5	32.9	509	2	O9RHG1	O9rhg1 bacillus ce
16	641.5	32.8	482	16	Q9XI68	Q9xi68 thermotoga

Q9hxm5	pseudomonas	17	632	32.3	489	16	Q9HXM5
Q9par5	xylella fas	18	629	32.2	485	16	Q9PAR5
Q9knu8	bacillus ha	19	628	32.1	485	16	Q9KGN8
Q9jud0	neisseria m	20	626	32.0	487	16	Q9JUD0
Q9jb25	neisseria m	21	625	32.0	487	16	Q9JB25
Q99w19	staphylococ	22	613	31.4	488	16	Q99W19
Q9rt87	deinococcus	23	606.5	31.0	500	16	Q9RT87
Q9ktw3	vibrio chol	24	600	30.7	489	16	Q9KTW3
Q9pkm2	chlamydia m	25	599.5	30.7	357	16	Q9PKM2
Q926y9	listeria in	26	597.5	30.6	488	16	Q926Y9
Q91017	streptomyce	27	586	30.0	501	2	Q91017
Q9rh20	corynebacte	28	577.5	29.5	506	2	Q9RH20
Q97n43	streptococc	29	574.5	29.4	492	16	Q97N43
Q9ciy6	lactococcus	30	570.5	29.2	493	16	Q9CIY6
Q9a7v2	caulobacter	31	565	28.9	487	16	Q9A7V2
Q97814	thermoplasm	32	558.5	28.6	485	17	Q978L4
Q92t5	rhizobium m	33	557	28.5	500	16	Q92RT5
Q983f6	rhizobium l	34	544	27.8	500	16	Q983F6
O26445	methanother	35	523.5	26.8	484	17	O26245
O9h1k8	thermoplasm	36	516.5	26.4	485	17	O9HLK8
O42831	saccharomyc	37	504.5	25.8	157	3	O42831
Q9hqu4	halobacteri	38	487.5	24.9	527	17	Q9HQU4
O2912	chlamydia p	39	434	22.2	246	16	O29212
O86844	streptomyce	40	411.5	21.0	523	2	O86844
Q9p3x8	schizosacch	41	395.5	20.2	148	3	Q9P3X8
Q9ybu2	aeropyrum p	42	394	20.2	444	17	Q9YBU2
O89058	mus musculu	43	375	19.2	82	11	O89058
Q92fc7	listeria in	44	373.5	19.1	502	16	Q92FC7
Q9kmw9	vibrio chol	45	354	18.1	347	16	Q9KMW9
Q91028	streptomyce	46	349.5	17.9	483	2	Q91028
Q9dcz1	mus musculu	47	348	17.8	345	11	Q9DCZ1
Q9p2t1	homo sapien	48	345	17.6	348	4	Q9P2T1
O92kz2	helicobacte	49	339	17.3	325	16	O92KZ2
Q99127	mus musculu	50	338	17.3	348	11	Q99127
O25525	helicobacte	51	335	17.1	327	16	O25525
Q97dk4	clostridium	52	335	17.1	327	16	Q97DK4
Q96hd6	homo sapien	53	335	17.1	345	4	Q96HD6
Q97ag5	streptococc	54	326.5	16.7	328	16	Q97AG5
O05269	bacillus su	55	325	16.6	326	16	O05269
Q9nj48	onchocerca	56	322.5	16.5	364	5	Q9NJD8
Q9cgf1	lactococcus	57	310	15.9	329	16	Q9CGF1
Q99qrl	streptococc	58	303	15.5	327	16	Q99QRL
Q99ud9	staphylococ	59	296	15.1	325	16	Q99UD9
O81282	prunus pers	60	288	14.7	116	10	O81282
P78758	schizosacch	61	285.5	14.6	232	3	P78758
Q91ca5	bacillus ha	62	250	12.8	281	2	Q91CA5
P73853	synchocyst	63	245.5	12.6	387	16	P73853
Q91016	streptomyce	64	218	11.2	374	2	Q91016
Q9c958	lactococcus	65	157	8.0	383	16	Q9CG58
O28109	archaeoglob	66	152	7.8	274	17	O28109
Q97da4	clostridium	67	151	7.7	310	16	Q97DA4
Q9a327	caulobacter	68	149.5	7.6	321	16	Q9A327
Q9rhy9	corynebacte	69	149	7.6	376	2	Q9RHY9
Q9kga2	bacillus ha	70	148.5	7.6	315	16	Q9KGA2
Q9nr9	leishmania	71	144.5	7.4	63	5	Q9NR9
Q9f8b8	carboxydoth	72	142	7.3	130	2	Q9F8P8
Q96gp9	homo sapien	73	141	7.2	165	4	Q96GP9
Q9a453	caulobacter	74	140	7.2	325	16	Q9A453
P71591	mycobacteri	75	138	7.1	322	16	P71591
Q9a7z7	caulobacter	76	136	7.0	311	16	Q9A7Z7
Q9rqd7	zymomonas m	77	134.5	6.9	334	2	Q9RQD7
Q914v0	pseudomonas	78	134	6.9	328	16	Q914V0
Q9f7p8	uncultured	79	133.5	6.8	322	2	Q9F7P8
Q929k2	listeria in	80	132.5	6.8	309	16	Q929K2
Q99yd4	streptococc	81	128	6.5	323	16	Q99YD4
Q9p635	neurospora	82	127.5	6.5	379	3	Q9P635
Q9fbc5	streptococc	83	127	6.5	324	16	Q9FBC5
Q93k07	lactobacill	84	126	6.4	366	2	Q93K07
Q9a5s5	caulobacter	85	122	6.2	335	16	Q9A5S5
Q92dk3	listeria in	86	120	6.1	309	16	Q92DK3
O22792	amycolatops	87	119.5	6.1	357	2	O22792
O29309	archaeoglob	88	119.5	6.1	511	17	O29309
Q97m06	clostridium	89	118.5	6.1	208	16	Q97M06

```
90 118 6.0 325 16 Q9K9K6 Q9K9K6 bacillus ha
91 116.5 6.0 198 16 Q9CCG2 Q9CGC2 lactococcus
92 116.5 6.0 358 2 Q939X9 Q939X9 amycolatops
93 116.5 6.0 365 10 Q9LJH3 Q9LJH3 arabidopsis
94 115 5.9 351 16 Q9HWH9 Q9HWH9 pseudomonas
95 114.5 5.9 333 10 Q9FMG0 Q9FMG0 arabidopsis
96 113.5 5.8 233 16 Q9T095 Q9T095 streptococc
97 113.5 5.8 363 10 Q9LJH5 Q9LJH5 arabidopsis
98 112 5.7 298 16 Q97FS7 Q97FS7 clostridium
99 111.5 5.7 442 16 Q986I0 Q986I0 rhizobium l
100 110 5.6 323 2 Q93QE0 Q93QE0 rhizobium m
```

ALIGNMENTS

```
RESULT 1
Q96NU2 PRELIMINARY; PRT; 489 AA.
AC Q96NU2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ30078.F15, CLONE BGC1200533, HIGHLY SIMILAR TO
DE INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE 2 (EC 1.1.1.205).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsui K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK054640; BAB70780.1; -
SQ SEQUENCE 489 AA; 52597 MW; 47A1273662A8C39B CRC64;
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Query Match 89.0%; Score 1740.5; DB 4; Length 489;
Best Local Similarity 74.6%; Pred. No. 1.le-122;
Matches 365; Conservative 5; Mismatches 14; Indels 105; Gaps 6;

Qy 1 MADYLISSGTVGVPEDGLTAQOLFASADGLTYNDFLILPGFIDFIDEVLTSAITRKIT 60
Db 1 MADYLISSGTVGVPEDGLTAQOLFASADGLTYNDFLILPGFIDFIDEVLTSAITRKIT 60

Qy 61 LKTPLISSPMDTVTADMAIAMA-----CTPEF-----QANEYRK--- 106
Db 61 LKTPLISSPMDTVTADMAIAMA-----CTPEF-----QANEYRK--- 106

Qy 84 ---LMGFI---IGFI---HNN-----HNN-----QANEYRK--- 106
Db 121 ETGTWGLKLVIGVTSRDIDFLAEKDHDTLLSEVMTPIRELVVAPAGVTLKEANEILQSK 180

Qy 107 -----VKKFDKTLCCGAAAGTREDOKYRDLTLQ 135
Db 181 KGLKPIVNDCELVIAIARTDLKKNRDYPLASKDA 240

Qy 136 AGVDVIVLDSSQNSVYQIAMVHYIKQYPHLQVIVLDSSQNSVYQIAMVHYIKQYPHLQV 195
Db 241 AGVDVIVLDSSQNSVYQIAMVHYIKQYPHLQVIVLDSSQNSVYQIAMVHYIKQYPHLQV 300

Qy 196 GCGSICITQEVNMACRPGCTAVYKVAEYARRFGVPIIADGGIQTQVGVVKKALALGASTVM 255
Db 301 GCGSICITQEVNMACRPGCTAVYKVAEYARRFGVPIIADGGIQTQVGVVKKALALGASTVM 360

Qy 256 MGSLLAANTEAPGEFFSDGVRLKRYRGMGLDAMEKSSSSQKRYFSEGDKVKYIAQGVSG 315
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Db 361 MGSLLAANTEAPGEFFSDGVRLKRYRGMGLDAMEKSSSSQKRYFSEGDKVKYIAQGVSG 420
Qy 316 STQDKSGTQKFPYPIAGIQHCQDQIGARSLSVLRSMYSGELKPEKRTMSAQIEGGVHG 375
Db 421 STQDKSGTQKFPYPIAGIQHCQDQIGARSLSVLRSMYSGELKPEKRTMSAQIEGGVHG 480
Qy 376 LHSYEKRLY 384
Db 481 LHSYEKRLY 489

RESULT 2
Q91Z11 PRELIMINARY; PRT; 514 AA.
AC Q91Z11;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INOSINE 5'-PHOSPHATE DEHYDROGENASE 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010314; AAH10314.1; -
SQ SEQUENCE 514 AA; 55815 MW; 17D25A5C5EBCC439 CRC64;
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Query Match 84.2%; Score 1646; DB 11; Length 514;
Best Local Similarity 63.6%; Pred. No. 1.5e-115;
Matches 327; Conservative 29; Mismatches 28; Indels 130; Gaps 1;

Qy 1 MADYLISSGTVGVPEDGLTAQOLFASADGLTYNDFLILPGFIDFIDEVLTSAITRKIT 60
Db 1 MADYLISSGTVGVPEDGLTAQOLFASADGLTYNDFLILPGFIDFIDEVLTSAITRKIT 60

Qy 61 LKTPLISSPMDTVTADMAIAMAALMGIGIFTHNCTPEFOANEVRKVKFFD----- 111
Db 61 LKTPLISSPMDTVTADMAIAMAALMGIGIFTHNCTPEFOANEVRKVKVKYEGGFTDPV 120

Qy 112 ----- 111
Db 121 LSPKDRVDFEAKARHGFQGIPTDTGTRGSLVGLIISRDIDFLKEEHDRPLEEIMT 180

Qy 112 ----- 111
Db 181 KREDLVAPAGVTLKEANEILQSKKGLPIVNDDELVAIARTDLKKNRDYPLASKDA 240

Qy 112 -KTLCCGAAGTREDOKYRDLTLQAGVDVIVLDSSQNSVYQIAMVHYIKQYPHLQV 170
Db 241 KKQLCCGAAGTREDOKYRDLTLQAGVDVIVLDSSQNSVYQIAMVHYIKQYPHLQV 300

Qy 171 GGNVYVTAQAANKLIDAGVGLRVGMCGSICITQEVNMACRPGCTAVYKVAEYARRFGVP 230
Db 301 GGNVYVTAQAANKLIDAGVGLRVGMCGSICITQEVNMACRPGCTAVYKVAEYARRFGVP 360

Qy 231 IADGGIQTQVGVVKKALALGASTVMGSLLAATTEAPGEYFFSDGVRLKRYRGMGLDAM 290
Db 361 IADGGIQTQVGVVKKALALGASTVMGSLLAATTEAPGEYFFSDGVRLKRYRGMGLDAM 420

Qy 291 EKSSSSQKRYFSEGDKVKYIAQGVSGIQDKSGIQKFPYPIAGIQHCQDQIGARSLSVLR 350
Db 421 DRHLSQQNRYFSEADKIKVAQGVSGAVQDKSGIHKFPYPIAGIQHCQDQIGARSLSVLR 480

Qy 351 SMYSGELKPEKRTMSAQIEGGVHGLHSHYEKRLY 384
Db 481 AMYSGELKPEKRTSSAQVEGSHSHSHYEKRLF 514
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RESULT 3
Q9DCL6 PRELIMINARY; PRT; 445 AA.
AC Q9DCL6;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE INOSINE 5'-PHOSPHATE DEHYDROGENASE 2.
GN IMPDH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK002676; BAB22278.1; -.
DR HSP; P12268; I330.
DR MGD; MGI:109367; Impdh2.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 445 AA; 48474 MW; 1B3A4006640CB4C9 CRC64;

Query Match 67.78; Score 1323; DB 11; Length 445;
Best Local Similarity 59.68; Pred. No. 2.3e-91;
Matches 265; Conservative 25; Mismatches 25; Indels 130; Gaps 1;

Qy 70 MDTVTEADMAIAMLGSGIGFIHNCIPEFOANEVRKVKFD----- 111
Db 1 MDTVTEAGMATAMALTGSGIGFIHNCIPEFOANEVRKVKYEQGFIPTPVVLSPKDRVD 60
Qy 112 ----- 111
Db 61 VFEAKARHFGCGIPITDTRGRMSRLVGLISSRDIDFLKEEHRFLBEIMTKREDLVVAP 120
Qy 112 -----KYLICGAA 119
Db 121 AGVTLKEANEILQRKSKGLPIVNVNDELVAIIARTDLKKNRDYPLASKDAKLLKLCAD 180
Qy 120 VGTREDDKYRLDLTQAGVDVIVLDSSQNSVYOIAMVHYIKOKYPHLOVIGGNVTTAAQ 179
Db 181 IGTTHEDDKYRLDLLALAGVDVIVLDSSQNSIFQINMIKIKYKIPSLQVIGGNVSCAQ 240
Qy 180 AKNLIDAGVDGLRGMCGSICITQEVNACGRPOGTAVYKVAEYARRFGVPITADGGTQT 239
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Db 241 AKNLIDAGVDALRVGMGSSICITQEVNACGRPOATAVYKVEYARRFGVPVITADGGIQN 300
Qy 240 VGHVVKALALGASTVMGSLAATTEAPGEYFFSDGVRLLKKYRGMSLDAMEKSSSSQKR 299
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 VGHAKALALGASTVMGSLAATTEAPGEYFFSDGIRLLKKYRGMSLDAMDHLSSONR 360
Qy 300 YFSEGDKVKIAQGVSGSIQDKSIQKFPVYLIAGIQHQCDIGARSLSVLRMMYSGELK 359
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 YFSEADKIKVAQGVSGAVQDKSGIHKFVYLIAGIQHQCDIGAKSLTQVRAMMYSGELK 420
Qy 360 FEKRTMSAQIEGGVHGLHSYEKRLY 384
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 FEKRTSSAQVEGGVHLSHSEKRLF 445
RESULT 4
Q9P8J2 PRELIMINARY; PRT; 521 AA.
AC Q9P8J2;
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE PUTATIVE INOSINE 5-MONOPHOSPHATE DEHYDROGENASE.
GN IMH3.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1006;
RX MEDLINE=20569171; PubMed=11119495;
RA Beckerman J., Chibana H., Turner J., Magee P.T.;
RT "Single-copy IMH3 allele is sufficient to confer resistance to
RT mycophenolic acid in Candida albicans and to mediate transformation of
RT clinical Candida species.";
RL Infect. Immun. 69:108-114(2001).
DR EMBL; AF249293; AAF70813.1; -.
DR HSP; P12268; I330.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
DR VARIANT 47 47 V -> I.
DR VARIANT 102 102 A -> S.
DR VARIANT 400 400 D -> G.
SQ SEQUENCE 521 AA; 56267 MW; 7A1CF4DF6184FE7E CRC64;
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Query Match 61.38; Score 1198.5; DB 3; Length 521;
Best Local Similarity 48.88; Pred. No. 6.7e-82;
Matches 247; Conservative 52; Mismatches 74; Indels 133; Gaps 3;

Qy 12 YVPEDGLTAQOLFASAD--GLTYNDPILILPGFIDFIADVDLTSAITKTLTKPLTSSP 69
| :||| :| :| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 15 YPKDKGSLVKELIDSTNFGGLTYNDLILPGLVNPFPSSAVSLETKTLTKITLSPFVSSP 74
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Qy 70 MDTVTEADMAIAMLGSGIGFIHNCIPEFOANEVRKVKFD----- 111
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 75 MDTVTEENMAIHMALGIGIHHNCIPEFOANEVRKVKYENGFINDPVVISPEVTIGE 134
Qy 112 ----- 111
Db 135 VKKMGVLGTFSPVVTENGKVGKLVGLIITSRDITQFHEDNKPVSVEYMTKDLVVGKKGIS 194
Qy 112 -----KYLICGAAVGT 122
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 195 LTDGNELLRSSKGLKPLIVDAEGLNLSLISRTDLQKQDYPNASKSFHKKOLLCGAAIGT 254
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Qy 123 REDDKYRLDLLTQAGVDVIVLSSSGNSVYQIAMVHYIKQKYPHLOVIGGNVTTAAQAKN 182
Db 255 IDADRLKLVEAGLDVVLSSSGNSVYQIAMVHYIKQKYPHLOVIGGNVTTAAQAKN 314
Qy 183 LIDAGVGLRVGMGCGSICITQEVWACGRPOGTAVYKVAEYARREGVPLIADGGIOTVGH 242
Db 315 LIEAGADALRIGMGSICITQEVWACGRPOGTAVYKVAEYARREGVPLIADGGIOTVGH 374
Qy 243 VVKALALGASTVMGSLAATTEAPGEYFFSDGVRLKRYKRGMSLDAMEK-----SSSSQK 298
Db 375 ITKALALGASVVMGSLAATTEAPGEYFFSDGVRLKRYKRGMSLDAMEK-----SSSSQK 434
Qy 299 RYFSEGDVKVIAQGVSGSQDKGSIQKFPVYLIAGIQHCGQDIGARSLVLSRMYSGEL 358
Db 435 RYFSEADKVLVAQGVSGSVVDKGSITKFPVYLYNGIQLSHQSLQDIGIKSIDELRENDNGEI 494
Qy 359 KFEKRTMSAQIEGGVHGLHSYEKRLY 384
Db 495 RFEFTASAQIEGGVHGLHSYEKRLH 520

RESULT 5
Q9UVL0 PRELIMINARY; PRT; 529 AA.
AC Q9UVL0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125226; PubMed=11232353;
RA Ye D., Lee C.H., Queener S.F.;
RT "Differential splicing of Pneumocystis carinii f. sp. carinii inosine
5'-monophosphate dehydrogenase pre-mRNA.;"
RL Gene 263:151-158(2001).
DR EMBL; AF196975; AAF13230.1; -.
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 529 AA; 58066 MW; 030573A8854ADB5A CRC64;

Query Match 58.5%; Score 1144; DB 3; Length 529;
Best Local Similarity 45.8%; Pred. No. 8.5e-78;
Matches 233; Conservative 58; Mismatches 82; Indels 136; Gaps 3;

Qy 12 YVPEDGLTAQQLFASA--DGLTYNDFLILPGFIDFADVDLTSALTRKILTKPLISSP 69
Db 20 YSEKGDYDLDSLCRRHGLYNDIILPGYIDFVNSVLSHITKIVLKTFFMSSP 79
Qy 70 MDTVTEDMAIAMALMGGIGTGFHHNCTPEFQANEVRKVKKFD----- 111
Db 80 MDTVTESDMAINALLGGIGTGFHHNCTIEEQTEMVRKVKKFFNGFTSPIVLSLNRHVRD 139
Qy 112 ----- 111
Db 140 VRRRIKEELGFGIPITDTGQLNGKLLGIVTSRDIQFHNNDESFLSEVMTKDLVTGSEGR 199
Qy 112 -----KTLCCGAAGVT 122
Db 200 LEEANEILRSCKGKLPIVDKEGNLTALLSRSDLMKLNHFLPLASKLPDSKQLICAAAGVT 259
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Qy 123 REDDKYRLDLLTQAGVDVIVLSSSGNSVYQIAMVHYIKQKYPHLOVIGGNVTTAAQAKN 182
Db 260 RPDDRIRKLHVEAGLDIVLSSSGNSIYQINMIKKKFFPNLEVIAGNVVTTREQAAN 319
Qy 183 LIDAGVGLRVGMGCGSICITQEVWACGRPOGTAVYKVAEYARREGVPLIADGGIOTVGH 242
Db 320 LISAGADALRVGMGSGSICITQEVWACGRPOGTAVYKVAEYARREGVPLIADGGIOTVGH 379
Qy 243 VVKALALGASTVMGSLAATTEAPGEYFFSDGVRLKRYKRGMSLDAMEKSSSSQK----- 298
Db 380 ITKALALGASVVMGSLAATTEAPGEYFFSDGVRLKRYKRGMSLDAMEHLSGKNKGDNA 439
Qy 299 ---RYFSEGDVKVIAQGVSGSQDKGSIQKFPVYLIAGIQHCGQDIGARSLVLSRMYMS 355
Db 440 ASSRYFGEADRTIRVAQGVSGSVVDKGSILHVVYPLRTGLQHSLOQDIGVQNLTELKQVKE 499
Qy 356 GELKFEKRTMSAQIEGGVHGLHSYEKRLY 384
Db 500 KNIRFEFTVASQLEGNVHGLDSYQKKLW 528

RESULT 6
O14344 PRELIMINARY; PRT; 524 AA.
AC O14344;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE PROBABLE INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
DE (IMP DEHYDROGENASE) (IMPDH) (IMPD).
GN SPC2F12.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (Jun-1997) to the EMBL/GenBank/DBJ databases.
CC - CATALYTIC ACTIVITY: INOSINE 5'-PHOSPHATE + NAD(+) + H(2)O =
XANTHOSINE 5'-PHOSPHATE + NADH.
CC - PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC - SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO GMP
REDUCTASE.
CC - SIMILARITY: CONTAINS 2 CBS DOMAINS.
DR EMBL; Z97211; CAB10161.1; -.
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
KW Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
Purine biosynthesis; Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT DOMAIN 182 236 CBS 2.
FT BINDING 337 337 IMP (POTENTIAL).
SQ SEQUENCE 524 AA; 57026 MW; E6C822C22E74674F CRC64;

Query Match 55.1%; Score 1076.5; DB 3; Length 524;
Best Local Similarity 44.1%; Pred. No. 1e-72;
Matches 224; Conservative 58; Mismatches 91; Indels 135; Gaps 3;

Qy 12 YVPEDGLTAQQLFASA--ADGLTYNDFLILPGFIDFADVDLTSALTRKILTKPLISSP 69
Db 17 YEKRDGLSIDDILRHNFQGLTFDFLILPGYIDFVPPNVSLETRISNVLKTPFMSSP 76
Qy 70 MDTVTEDMAIAMALMGGIGTGFHHNCTPEFQANEVRKVKKFD----- 111
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Db 77 MDTVTEDQMALYALLGGIGVHHNCTPEQAAAMVRKVKYENGFIIDPVPVFSPOHTVGD 136
Qy 112 ----- 111
Db 137 VLKIKETKGFSGIPITENGLKRGKLVGIVTSRDVQFHKDTNPVTEVMTPREELITTAEG 196
Qy 112 -----KTLCCGAAY 120
Db 197 ISLERANEMLRKSKKGLPVVDKDDNLVALLSLTDLAKNLHFLPLAKTSOTKQLMVAARI 256
Qy 121 GTRDDKYRLDLLTQAGVDVIVLSSQGSNVYQIAMVHYIKQKYPHQLVIGGNVYTAQA 180
Db 257 GTRDDRTRLALLAAGIDAVVIVLSSQGSNCFQIEMIKWKIKTKPKIDVIAGNVVTRQT 316
Qy 181 KNLIDAGVGLRVMGCGSICITEVMACGRPQGTAVYKVAEYARRGVPVLIADGGIOTV 240
Db 317 ASLIAAGADGLRVMGCGSACITEVMACGRPQGTATAAQVAEFAAQFGIGVIADGGIQNV 376
Qy 241 GHVYKALAGASTVMGSLLAATTEAPGEYFFSDGVRLLKRYGMGSLDAME-----KSSSS 296
Db 377 GHVYKSLSGATAVMGSLLAGTTESGEYVYVREGQRYKSYRGMSIAAMEGTGVNKNAS 436
Qy 297 QKRYFSGDKVYKIAQVSGSIQDKGSIQKVPYPIYLIAGIQHGCODIGARSLSVLSRMYSG 356
Db 437 TGRYFSENDVAVRQVSGVGLVVDKGLRLLRPLPYLTGLQHALQDGTGKSLDELHEAVDKH 496
Qy 357 ELKPEKRTMSAQIEGGVHGLHSYEKRLY 384
Db 497 EVRFELKSSAAIREGDIQGFATYEKRLY 524

RESULT 7
Q9GZH3 ID Q9GZH3 PRELIMINARY; PRT; 499 AA.
AC Q9GZH3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE T22D1.3 PROTEIN.
GN T22D1.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Geisel C., Bradshaw H., Hawkins M.;
RT "The sequence of C. elegans cosmid T22D1.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RL EMBL: AF039052; AAF98635.1; -
DR HSSP; P12268; I830.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
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DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 499 AA; 54298 MW; E96323563FE5D275 CRC64;

Query Match 53.2%; Score 1039.5; DB 5; Length 499;
Best Local Similarity 43.9%; Pred. No. 5.7e-70;
Matches 221; Conservative 55; Mismatches 72; Indels 155; Gaps 5;

Qy 16 DGLTAQOLFASADGLTYNDFLILPGFIDFTADEVDLTSALTRKLTTLKTPLISSPMNVTE 75
Db 18 DGETVHEMMAHKAAGLTYNDFNLPGFINGVHDVSLNETITKDKIKAPLVSSPMNVTE 77
Qy 76 ADMAIAMAALMGGICFIHNC-TPEFQANEYRVKVKF-----DRT----- 113
Db 78 SGMAIVNALYGGIGIIHGNEPKPEDQAEVLKVRFKQYVMQPHCLSRDSTAFDMLQIK 137
Qy 114 ----- 113
Db 138 KKYGYTGAPVTEDEGRVSKLIGMVTSRDFDFTMDVAGOKGTPISDIMSVYDQLHLGHIN 197
Qy 114 -----LLCGAAY 121
Db 198 DAPLSOKKLKEHRLKGLPIVNDNGELCALLCRSDLKARDYPMASTDYDSKQLLCCGAAY 257
Qy 122 TREDDKYRLDLLTQAGVDVIVLSSQGSNVYQIAMVHYIKQKYPHQLVIGGNVYTAQA 181
Db 258 TRGESQYTVDRVVEAGVDVLIIDSSNGSSTYQISMLRYIKEKHPHVQVAGNVVTRAQAK 317
Qy 182 NLIDAGVDGLRVMGCGSICITEVMACGRPQGTAVYKVAEYARRGVPVLIADGGIOTV 241
Db 318 LLIDQAGADGLRVMGCGSICITEVMACGRPQGTAVYKVAEYARRGVPVLIADGGIOTV 377
Qy 242 HVYKALAGASTVMGSLLAATTEAPGEYFFSDGVRLLKRYGMGSLDAMEKSSSSQKRYF 301
Db 378 YIKALISLASAVNMGGILAAATTEAPGEYFWGPG-----GSFN-----F 416
Qy 302 SEGDKVIAQVSGSIQDKGSIQKVPYPIYLIAGIQHGCODIGARSLSVLSRMYSGELKFE 361
Db 417 SESDQIKVAQVSAATMDKRGSKHFIPYLTIRGVQHGMDIGVRSRDRFREKVDNGIVKFE 476
Qy 362 KRTMSAQIEGGVHGLHSYEKRLY 384
Db 477 RRTNAQLGEGVHLSHSEKRLY 499

RESULT 8
Q9ZPAO ID Q9ZPAO PRELIMINARY; PRT; 502 AA.
AC Q9ZPAO;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INOSINE MONOPHOSPHATE DEHYDROGENASE.
GN IMPDH1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC Cao Y., Schubert K.R.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010201; CAB38030.1; -
DR HSSP; P12268; I830.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 502 AA; 53407 MW; 617AB87613C36AA4 CRC64;
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	Qy	147	CGNSVYQTAMVHYIKQKYPHQLQVIGNVVVTAQAANKLIDAGVDGLRVGMGCGSICITQEV	206
	Dt		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
	Db	250	HGSQGVLEAVKTIKKAYPELQVIAGNATAAAVAHVHDLTAEAGADCVKVGIGPGSICTTRVV	309
	Qy	207	MACGRPOGTAVYKVAEYARRRGCVPIIADGGTQTGVHVVKALGAALGASTVMGSLAATTEA	266
	Db	310	AGIGVPQLTAVMCDVEEANKYGVPIIADGGTKISGDIVKALAAGA KAKAVMMGSMFAGCBEA	369
	Qy	267	PGEYFFSDGVLRLKYRGMGSLDAMEKSSSKRYRFSEGDVKYIAQGVSGSIQDKGSIQKF	326
	Db	370	PGETEIYQGRSYKYVRGNGSLAAHQ--CGSKDRYFQEGNKILVPEGEVRPFKGSVLET	427
	Qy	327	VPLYIAGIQHCQDIGARSLSVLRSMMYSGLKFKPRTMSAQIEGGVYHGLHSYE	380
	Db	428	VFOILGIRSGMGYLGRSNMTET-----FEKATFVVQTSAGLRSHPHD	471
	RESULT	13		
	Q9PNN3		PRELIMINARY; PRT; 485 AA.	
	ID	Q9PNN3		
	AC	Q9PNN3;		
	DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
	DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
	DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
	DE	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205).		
	GN	GUAB OR CJI058.		
	OS	Campylobacter jejuni.		
	OC	Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;		
	OX	Campylobacter.		
	NCBI_TaxID	-197;		
	RN	[1]		
	RP	SEQUENCE FROM N.A.		
	RC	STRAIN=NCTC 11168;		
	RA	MEDLINE=20150912; PubMed=10688204;		
	RA	Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,		
	RA	Basham D., Chillingworth T., Davies R.M., Felkwell T., Holroyd S.,		
	RA	Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,		
	RA	Quail M.A., Rajandream A.M., Rutherford K.M., van Vliet A.H.M.,		
	RA	Whitehead S., Barrell B.G.;		
	RT	"The genome sequence of the food-borne pathogen Campylobacter jejuni		
	RL	reveals hypervariable sequences.";		
	Nature	403:665-668(2000).		
	DR	EMBL; ALJ39077; CAB73314.1; -		
	DR	HSP; PL2268; I830.		
	DR	InterPro; IPR000644; CBS.		
	DR	InterPro; IPR003009; FMN_enzyme.		
	DR	InterPro; IPR001093; IMP_DH_GMP_RED.		
	DR	Pfam; PF00571; CBS; 2.		
	DR	Pfam; PF00478; IMPDH_C; 1.		
	DR	Pfam; PF01574; IMPDH_N; 1.		
	DR	SMART; SM00116; CBS; 2.		
	DR	PROSITE; PS00487; IMP_DH_GMP_RED; 1.		
	KW	Complete proteome.		
	SQ	SEQUENCE 485 AA; 52151 MW; 634332666B963CDF CRC64;		
	Query Match	33.5%; Score 654.5; DB 16; Length 485;		
	Best Local Similarity	34.5%; Pred. No. 4.8e-41;		
	Matches	165; Conservative 57; Mismatches 107; Indels 149; Gaps		8;
	Qy	30	LTYNDFLLLPGFDIFADIADVDLTSLNPKITLKTPLISSPMDTVTEDMATAMMGIG	89
	Db		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
	Db	8	LTFDEVLLRPGYSEVLPKEVRIHKTLKNITLNPLISAAMDVTVEHRAAIMMARLGIG	67
	Qy	90	FIHINCTPEFOANERVKKFF-----DK	112
	Db		I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	
	Db	68	VIHRNMDSOVREVRKVKKSSEGVIIPIFVPSKASVAEALEIMAEYRISGVPPVDEDK	127
	Qy	113	TLL-----	115
	Db		I :	
	Db	128	KLIGLTNRDLRFESDFSNLVENVMTKMPLITAPKGCTLDDAEKIFSTNKVEKLPVDEQ	187

Qy	116	-----CGAAGVTREDDKVRLLDITQAGVDVIVLDS	145
Db	188	GRLEGLITIKDKRRKKEYPDANKDNFGRLRGAAIGVGQMD--RVDALVEAGVDVVVLDS	245
Qy	146	SOGSNVYQIAWVHYIKOKYPHLQVIGNVVYTAQAOKNLIDAGVDGLRVGMGCGSICITQE	205
Db	246	AHGSHKGIIDTVKAIRKAKYPNLIDLAGNIATAAAKALCEAGVDVAVKVGIGPGSICITRI	305
Qy	206	VMACGRPQGTAVYKVAEYARRFGVPIIADGGIQTGVHVVKALGALGASTVNMGSLLAATTE	265
Db	306	VSGVGVPQISNAIDECVEANKFGVPVIADGGIKYSGDIKALAVGASSVMIGSLLACTDE	365
Qy	266	APGEYFFSDGVRLLKKYRGMGSLDAMEKSSSSQKRYFSEG---DKVKIAQGVSGSIQDKGS	322
Db	366	SPGELFTYQGRQYKSYRGMGSLGAMQKGSSD--RYFQOQTAQDKL-VPEGIEGRVFPVGS	422
Qy	323	IQKFPVYLIIAGIQHCQDIIAGRSLSVLRSMMYSGELKFEKRTMSAQI-----EGGVH	374
Db	423	IRSVYHLLGLLRSSMGVYGAKDIE-----DFQKRAEFVEITTAGLKESHVH	469
RESULT	14		
Q9R9HG9			
ID	Q9R9HG9	PRELIMINARY; PRT; 509 AA.	
AC	Q9R9HG9		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)		
DE	IMP DEHYDROGENASE.		
GN	IMPDH.		
OS	Bacillus cereus.		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;		
OC	Bacillus/Staphylococcus group; Bacillus.		
OX	NCBI_TaxID=1396;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=TS-4;		
RA	Kim S., Miyamoto T., Honjoh K., Iio M., Hatano S.;		
RT	Molecular cloning, Overproduction and Characterization of the		
RT	Bacillus cereus IMP dehydrogenase.";		
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB035643; BAA88235.1; -		
DR	HSSP; P50099; 1zFJ.		
DR	InterPro; IPR000644; CBS.		
DR	InterPro; IPR003009; FMN_enzyme.		
DR	InterPro; IPR001093; IMP_DH_GMP_RED.		
DR	Pfam; PF00571; CBS; 2.		
DR	Pfam; PF00478; IMPDH_C; 1.		
DR	Pfam; PF01574; IMPDH_N; 1.		
DR	SMART; SM00116; CBS; 2.		
DR	PROSITE; PS00487; IMP_DH_GMP_RED; 1.		
SQ	SEQUENCE 509 AA; 55393 MW; 9E6ACB3872C4A451 CRC64;		

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Query Match      33.2%; Score 649; DB 2; Length 509;
Best Local Similarity 35.0%; Pred. No. 1.3e-40;
Matches 157; Conservative 50; Mismatches 114; Indels 128; Gaps 3;

QY      28 DGLYNDFLILPGIFDFTADEVDLTSALTRKTLTKPLTISSPMDTVTEADMAIAMLGG 87
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      9 EGLTFDVLIVPARSDILPREVSKTVLSELSQLNIPLISAGMDTVTEADMAIAROGG 68

QY      88 IGFTHNCTPEFOANVRKVK----- 108
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      69 LGIITHKNMSIEQAEQVDQVKVRSEGSVIDPFLTPEHQVYDAEHLMKYRISGVPVNN 128

QY      109 -----KFDK--- 112
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      129 LDERKLVGITNRDMRFIQDYIKISDVTWYEQLTIPAVGTTLEAEKILOKYIEKLP 188

QY      113 -----TLCCGAAGVTREDDKYRLDLTLTQAGVDVI 141
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      189 VDNNGVLOGLTIIKDIEKIVFEPNSAKDKGRLVGAAGVYTADAYLRIDALVRASVDAI 248

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Db 183 SKDNKLVGTTIKDMSVIEHPNNAERKRLVLGAAVGTSPETMBRVERKLVKAGVDVIV 242
QY 143 LSSOGNSVYQIAMVHYIKQYPHLQVIGNVVTAQAQKLNLDAGVGLRVGMGCGSICI 202
Db 243 IDTAHGSRRVETLEMIKADYDLPVAVGNATPCTEALIKAGADAVKVGPGSICT 302
QY 203 TOEVMACRPOGTAVYKVAEYARRFGVPIIADGGIQTGVHVVKALGALGASTVMGSLAA 262
Db 303 TRVAVGVGPQLTAVMECSVARKYDVPDIADGGIRYSGDIVKALAAAGAESVNVGSI 362
QY 263 TTEAPEYFESDGVRLKKYRGMSLDAMEKSSSQKRYFSEGDYKVIAGVSGSIDKGS 322
Db 363 TEAPGETILYQGRKYKAYRGMSGLAMR--SGSADRYQOEGENKFPVPEGIMVPYKGT 420
QY 323 IOKFPVYLIAGIQHGQDQIGARSLVSRMYSGLKFEKRTMSAQIEGVHGLHSYE 380
Db 421 VKDVHQLVGLRSGMYIGARTIKELQ-----EKAVFVKITPAGVKESHPHD 468

RESULT 17
Q9HXM5 PRELIMINARY; PRT; 489 AA.
AC Q9HXM5;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
GN GUAB OR PA3770.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.J., Gollery L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RA opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004796; AAG07157.1; -.
DR HSSP; P49058; 1EEP.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 489 AA; 51707 MW; 6D2320AFD52C888B CRC64;

Query Match 32.3%; Score 632; DB 16; Length 489;
Best Local Similarity 33.4%; Pred. No. 2.4e-39;
Matches 159; Conservative 55; Mismatches 130; Indels 132; Gaps 4;

QY 26 SADGLTYNDFILPGFDIFADVDLTSALRTKTLKTPLISSPMDTVTEADMAIAML 85
Db 5 SQEALTFDDVLLPGYSEVLPKDVSLKTLRTGLIELNPLVSAAMDVTEARLAIAKQE 64
QY 86 GGIGIHHNCTPEFOANEVRKYKFD----- 111
Db 65 GGIGIHHNMGIEQAAAEVRKYKHTAIVRDPVTVTPSTKIQLLOMAREYGFSGFPV 124
QY 112 ----- 111
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Db 125 EOGELVIGVTGRDLRVKPNAGDTVAAMTPKDKLVTAAREGTPLEEMKAKLYENRIEKMVL 184
QY 112 -----KT-----LIGAAVGTREDDKYRLDLLTFOAGVDVI 141
Db 185 VDENVYLRGLVTFRIEAKKATYPLASKDQGRRLRVGAAGTADTGTERVAALVAAGVDV 244
QY 142 VLDSSOGNSVYQIAMVHYIKQYPHLQVIGNVVTAQAQKLNLDAGVGLRVGMGCGSICI 201
Db 245 VYDTAHGHSKGVIERVVRVKQTFPDVQVIGGNATIAEAAKALAAAGADAVKVGIPGSI 304
QY 202 ITQEVWACRPOGTAVYKVAEYARRFGVPIIADGGIQTGVHVVKALGALGASTVMGSL 261
Db 305 TTRIVAGVGPVQISAIANVAALAEGLTGVPLIADGGIRFSGDLAKAMVAGAYCVMMG 364
QY 262 ATTEAPGEVFFSDGVRLKKYRGMSLDAMEKSSSQKRYF---SEGDKVIAQGVSGSI 318
Db 365 GTEAPGELELFGRSYKSYRGMSGLGAMSGSGSDRFDQASAGAELVPEGIEGRVP 424
QY 319 DKSGIQKFPYLIAGIQHGQDQIGARSLVSRMYSGLKFEKRTMSAQIEGVH 374
Db 425 YKGALSIVHQLMGLRAAMGYTGSADIQOMRT-----QPQFVRITGAGMAESHVH 475

RESULT 18
Q9PAR5 PRELIMINARY; PRT; 485 AA.
AC Q9PAR5;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
GN XF2430.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohelsel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshukako M.H.,
RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159(2000).
DR EMBL; AE004052; AAF85229.1; -.
DR HSSP; P49058; 1EEP.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
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DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 485 AA; 52188 MW; 8D20307B24FAAB90 CRC64;

Query Match      32.2%; Score 629; DB 16; Length 485;
Best Local Similarity 33.3%; Pred. No. 4e-39;
Matches 158; Conservative 61; Mismatches 121; Indels 134; Gaps 5;

QY 27 ADGLTYNDFILPFGIDFIDAEVDLTSAITRKITLTKPLTSSPMDVTVEADMAIAMAALMG 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 AEALTYDDVSLVSHSTVLPKDVNLETRNLRLKLPVLSAAMDVTVEARLAIVMAQLG 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 87 GIGFIHNCTPEFQANVRKVKFDK----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 GIGIHKNLTIQQVAETVKVKEYSGVIRDPITVPDTPETSIRDVLAALTRAKNISGVPPVD 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 ----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 KGQILGLVTHRDMRFESELDPPVRHIMTKKEALVTYVKEGADSQEVQLLHKHRIEKLTV 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 ----- 142
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 NDAPELRGLITVKDIQKSDYPNAAKDAVTVLLVGAAGVGGETERRVEITLAAAGVDVII 245
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 143 LDSQGSNVYQIAMVHIKQYKPHLVIGNVVTAQAQKNLIDAGVDGLRVGMCGSGICIT 202
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 246 VDTAHGYSQGVLDRAVAMIKRYFPQLQYVIGNVTDAAALMDAGADAVKVGVPGSICT 305
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 203 TOEYMACGRPQGTAVYKVAEYARFVPIITADGGIQTGVHVVKALALGASTVMGSLAA 262
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 306 TRMVAGVGPQITAVQVMSD-ALQDRPLIADGGIRYSGDIGKALAAAGASTVMIGGLFAG 364
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 263 TTEAPGYEYFSDGVRLKRYGMSGLDAMEKSSSKRYFSEGDKV--IAQGVSGSTQDK 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 365 TTEAPGDVELFOGRTYKSYRGMSLAAMEK--GSKDRYFOEASDVLDKLPGEIGRVPYR 422
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 321 GSIQKFPYLIAGIQHCQDQIGARSLVLSRMYSGELKFEKRTMSAQIEGVH 374
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 GSVSGIVHQLMGLLRATMGVYGVCATIEEMRT-----RPQFVKITGAGQGVESHVH 471
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 19
Q9KGN8 PRELIMINARY; PRT; 485 AA.
AC Q9KGN8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INOSITOL-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205).
GN GUAB OR BH0020.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=96665;
RN [1]
RP "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001507; BAB03739.1; -.
DR HSP; P50099; IZPJ.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
```

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DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 485 AA; 52429 MW; DOB64489E5CF8B60 CRC64;

Query Match      32.1%; Score 628; DB 16; Length 485;
Best Local Similarity 32.2%; Pred. No. 4.7e-39;
Matches 155; Conservative 66; Mismatches 122; Indels 138; Gaps 5;

QY 28 DGLTYNDFILPFGIDFIDAEVDLTSAITRKITLTKPLTSSPMDVTVEADMAIAMAALMG 87
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 EGLTFDDVLLVPAKSEVLPRDVSVKTKLTETLQNLNIPILISAGMDVTVEAKMAIAIEGG 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 88 IGFIHNCTPEFQANVRKVK-----FDK----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 69 LGIHKNSVEEQAEQVDVRKSESGVITNPFFLTDPDQVFEADHLMGKYRISGVPIVDE 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 ----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 129 DQKLVLGILTRDLRFTEDYSTLIDDDVMKTNLVTPYGTTLKEABEILQKHIEKLPLVD 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 ----- 143
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 189 ESGTLKGLITIKIEKVIETFPNSAKDSQGLIVGAAGVSAADTVRVAALVEAGVDVVI 248
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 144 DSSQGSNVYQIAMVHIKQYKPHLVIGNVVTAQAQKNLIDAGVDGLRVGMCGSGICIT 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 249 DTAHGSHKGVLEKVKALIREQYPDLTIIAGNVATAEATRDLEAGANVVKVIGPGSICIT 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 204 QEVMACGRPQGTAVYKVAEYARFVPIITADGGIQTGVHVVKALALGASTVMGSLAA 263
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 309 RIVAGIGVPOITAVYDCANEARKHGPVPIIADGGIKYSGSDIVKALAAAGHVMGLSLAGV 368
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 264 TEAPGYEYFSDGVRLKRYGMSGLDAMEKSSSKRYFSEGDKVVKIAQGVSGSIQDKGI 323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 369 SESPEEREIFQGRQFVKYRGMSLGAMEK--GSKDRYFOENNKLVPEGIEGRIPYKGL 426
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 324 QKFPYLIAGIQHCQDQIGARSLVLSRMYSGELKFEKRTMSAQIEG-GVHGLHSYEKR 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 427 HDTIHLVGGIRAGMGYCGTKTIDLR-----ENTQFTRITGAGLRSHPHDVQ 475
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 383 L 383
Db 476 I 476

RESULT 20
Q9JUD0 PRELIMINARY; PRT; 487 AA.
AC Q9JUD0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205).
GN GUAB OR NMAL372.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,
RA Jajels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
```

"Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491.";

RA Nature 404:502-506(2000).
 RA EMBL; AL162755; CAB84618.1; -.
 DR HSSP; P49058; 1EEP.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN_enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 DR Oxidoreductase; Complete proteome.
 KW OXIDOREDUCTASE; Complete proteome.
 SQ SEQUENCE 487 AA; 52367 MW; 984D41356B913BCB CRC64;

Query Match 32.0%; Score 626; DB 16; Length 487;
 Best Local Similarity 32.7%; Pred. No. 6.7e-39;
 Matches 155; Conservative 59; Mismatches 122; Indels 138; Gaps 6;

QY 31 TYNDFLLPGFDFTADEVDLTSALTREITKLTPLISSPMDVTVEADMAIAMLGGIGF 90
 DB 9 TDDVLLVPAHSTVLPDVKLTREITLNLPLLSAAMDVTVEARLAISNAQEGGIGI 68
 QY 91 IHNCTPEQANEVRKVKFD-----
 DB 69 IHKNMPPMQARAIKVRHESGVVDPVTVAPTTLIREVLEMRQAKRKMSGLPVVENG 128
 QY 112 -----
 DB 129 KVGIVTNRDLRFENRDLPSAINTPRELVTVPETGTSIDARELMHTHKVERVLVNE 188
 QY 112 -----KT-----LLCGAAVGTREDDKYRLDLITQAGVDVIVD 144
 DB 189 KDEKGLITVKDILKTEFPNANKDSEGLRVGAAGVGGDTEERVKALVEAGVDVIVD 248
 QY 145 SQGNSVQIAMVHIKQYPHLVGNVTAQAQKNIIDAGVDGLRVGMCGGICITQ 204
 DB 249 TAGHSQGVDRVVRWKETYPHIQVIGGNIAAKALDLVAAGADAVKVGIGPGSICITR 308
 QY 205 EVMACRPGGTAVYKVAEYARFVPIIADGGIQTGVHVVKALALGASTVMGSLAATT 264
 DB 309 IVAGVGPQLTAIHNVAEALKTGVPLIADGGIRFSGDIATAKALAGAYSVMLGGMPAGTE 368
 QY 265 EAPGEYFFSDGVRLLKRYRGMGSLDAMEKSSSSQKRYFSE---GDKVKIAQGVSGSIQDK 320
 DB 369 EAPGEIELYQGRSYKSYRGMGSLGM--SQGSADRYFQDKTDSADKY-VPEGIEGRVPYK 425
 QY 321 GSIOKFVPLYIAGIOHGGODICARSLSVLRSMYSGELKFKRTMSAQIEGVH 374
 DB 426 GPIVNIHQLTGGLRSSMGYLGCANIAEMHE-----KAEFVEITSAGMSSESHVH 474

RESULT 21
 Q9JZB5 ID Q9JZB5 PRELIMINARY; PRT; 487 AA.
 AC Q9JZB5;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE IMP DEHYDROGENASE.
 GN NMB1201.
 OS *Neisseria meningitidis* (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.
 OX NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisen J.A., Ketchum K.A., Hood D.W., Pedersen J.F., Dodson R.J.,
 Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
 Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
 Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.";
 RL Science 287:1809-1815(2000).
 DR EMBL; AE002468; AAF41583.1; -.
 DR HSSP; P49058; 1EEP.
 DR TIGR; NMB1201; -.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN_enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 DR Complete proteome.
 KW COMPLETE PROTEOME.
 SQ SEQUENCE 487 AA; 52383 MW; 4854B9C2681A2464 CRC64;

Query Match 32.0%; Score 625; DB 16; Length 487;
 Best Local Similarity 32.9%; Pred. No. 8e-39;
 Matches 156; Conservative 58; Mismatches 122; Indels 138; Gaps 6;

QY 31 TYNDFLLPGFDFTADEVDLTSALTREITKLTPLISSPMDVTVEADMAIAMLGGIGF 90
 DB 9 TDDVLLVPAHSTVLPDVKLTREITLNLPLLSAAMDVTVEARLAISNAQEGGIGI 68
 QY 91 IHNCTPEQANEVRKVKFD-----
 DB 69 IHKNMPPMQARAVSKVRHESGVVDPVTVAPTTLIREVLEMRQAKRKMSGLPVVENG 128
 QY 112 -----
 DB 129 KVGIVTNRDLRFENRDLPSAINTPRELVTVPETGTSIDARELMHTHKVERVLVNE 188
 QY 112 -----KT-----LLCGAAVGTREDDKYRLDLITQAGVDVIVD 144
 DB 189 KDEKGLITVKDILKTEFPNANKDSEGLRVGAAGVGGDTEERVKALVEAGVDVIVD 248
 QY 145 SQGNSVQIAMVHIKQYPHLVGNVTAQAQKNIIDAGVDGLRVGMCGGICITQ 204
 DB 249 TAGHSQGVDRVVRWKETYPHIQVIGGNIAAKALDLVAAGADAVKVGIGPGSICITR 308
 QY 205 EVMACRPGGTAVYKVAEYARFVPIIADGGIQTGVHVVKALALGASTVMGSLAATT 264
 DB 309 IVAGVGPQLTAIHNVAEALKTGVPLIADGGIRFSGDIATAKALAGAYSVMLGGMPAGTE 368
 QY 265 EAPGEYFFSDGVRLLKRYRGMGSLDAMEKSSSSQKRYFSE---GDKVKIAQGVSGSIQDK 320
 DB 369 EAPGEIELYQGRSYKSYRGMGSLGM--SQGSADRYFQDKTDSADKY-VPEGIEGRVPYK 425
 QY 321 GSIOKFVPLYIAGIOHGGODICARSLSVLRSMYSGELKFKRTMSAQIEGVH 374
 DB 426 GPIVNIHQLTGGLRSSMGYLGCANIAEMHE-----KAEFVEITSAGMSSESHVH 474

RESULT 22
 Q99WI9 ID Q99WI9 PRELIMINARY; PRT; 488 AA.
 AC Q99WI9;
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE INOSITOL-MONOPHOSPHATE DEHYDROGENASE.
 GN GUAB OR SA0375 OR SAV0390.
 OS *Staphylococcus aureus* (strain N315), and
Staphylococcus aureus (strain Mu50).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; *Staphylococcus*.


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OX NCBI_TaxID=158879, 158878;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR ENBL; AP003130; BAB41602.1; -.
DR ENBL; AP003359; BAB56552.1; -.
DR HSSP; P50099; 1ZFU.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 488 AA; 52850 MW; C4E945D25D41491D CRC64;

Query Match 31.4%; Score 613; DB 16; Length 488;
Best Local Similarity 32.4%; Pred. No. 6.4e-38;
Matches 154; Conservative 59; Mismatches 129; Indels 134; Gaps 5;

QY 28 DGLRYNDFLLPGIDFIDAEVDLTSALTTRKTLTKPLISSPMDTVTEADMAIAMALMG 87
DB 9 ESLTFDVLIPAGSDLPKDVLSQVLSKVNIPVISAGMDTVTESKMAIAMAROGG 68
QY 88 IGFTHHCTPEFOANEYRKVK-
DB 69 LGVIHKNMGVEEQADEVQKRSNGVISNPFPLTPEESYEAALMKYRISGVPIVDN 128
QY 109 -----KFDK--- 112
DB 129 KEDRLVGLTNRDLRFEDFSIKIVDMTOENLITAPVNTLLEAEKILQKHIEKLPL 188
QY 113 -----TLLCGAAGVTREDDKYRLDLLTQAGVDVIV 142
DB 189 VKDGRLEGLTIKDIEKVIPEPNAKDEHGRLLVAAAIGISKDTDIRAQKLVEAGVDVIV 248
QY 143 LDSSQGSNVIQIAMVHIKQYPHLQVIGNVVTAQAQAKNLIDAGVDGLRVGMCGSICI 202
DB 249 IDTAHGSKGVIDQVKHKKTYPEITLVAGNVATAETKDLFEAGADIVKVGIGPGSICT 308
QY 203 TOEWMACGRPGGTAVYKVAEYARFVGPIIADGGIQTGVHVVKALALGASTVMGSLAA 262
DB 309 TRVAVGVGPQITAIYDCATEARKHGKAILADGGIKFSGDIIKALAAGGHAVMLGSLAG 368
QY 263 TTEAPGEFFSDGVRLLKRYRGMSLDAMEKSSSQKRYFSEGDKV-IAQVSGSIOQK 320
DB 369 TEESPGATEIFQGRQYKYVRGMSLGAMEKGSND--RYFQEDKAPKRVFPEGIGRTAYK 426
QY 321 GSIQKFPYLIAGIOHGQCDIGARSLSVLRSMYSGLKFKRKTMSAQIEGVHGL 376
DB 427 GALQDTIYQLMGVVRAGMGYTGSHDLRELRE-----EAQFTRMPAGLAESHPHNI 477

RESULT 23
Q9RT87 PRELIMINARY; PRT; 500 AA.
AC Q9RT87;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
GN DR1878.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=RL;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RL";
RL Science 286:1571-1577(1999).
DR ENBL; AE002027; AAF11432.1; -.
DR HSSP; P49058; 1EEP.
DR TIGR; DR1878; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 500 AA; 53141 MW; 4351BC91B675A0D2 CRC64;

Query Match 31.0%; Score 606.5; DB 16; Length 500;
Best Local Similarity 30.7%; Pred. No. 2e-37;
Matches 145; Conservative 70; Mismatches 126; Indels 131; Gaps 4;

QY 28 DGLRYNDFLLPGIDFIDAEVDLTSALTTRKTLTKPLISSPMDTVTEADMAIAMALMG 87
DB 25 EGITFDVLLQPRISQVLPHEVDVSAQLTRVRLNIFVSAMDTVTETNAIAMAREGG 84
QY 88 IGFTHHCTPEFOANEYRKVKFKDKTL-
DB 85 IGVVHKNSIDAQAEMIRKVKRSSEGMIVDPTLPPSATVRDADRLMGEYRISGVPTAP 144
QY 116 ----- 115
DB 145 DGKLLGITNRDMRFIDDLVPLGDVMTREHLVTPVGTDLLEQARELFKLNRIEKLIVTE 204
QY 116 -----CGAAVGTREDDKYRLDLLTQAGVDVIVLD 144
DB 205 GEYLRGLITIKDIEKSVKYPNAAKDDLGRVAAAGVSADMDRAGALVORGADVLIVD 264
QY 145 SSQGSNVIQIAMVHIKQYPHLQVIGNVVTAQAQAKNLIDAGVDGLRVGMCGSICITQ 204
DB 265 SAHGSQGLNALSrvKEQF-DVDIAGNVATRSRGARDLILAGADAVKVGIGPGSICITR 323
QY 205 EVMACGRPGGTAVYKVAEYARFVGPIIADGGIQTGVHVVKALALGASTVMGSLAAT 264
DB 324 VVTGVGPQVTAIFEASAAAAMEAGIPVADGGIKQTDGVPKAIAGAASVVMGMSLAGTD 383
QY 265 EAPGEYFSDGVRLLKRYRGMSLDAMEKSSSQKRYFSEGDKVIAQVSGSIOQKSIQ 324
DB 384 EAPGETILDRGRYKYSRGMSLGAMGGSAD--RYFGGSRKRVFPEGIGIIRGTAG 441
QY 325 KFPYLIAGIOHGQCDIGARSLSVLRSMYSGLKFKRKTMSAQIEGVHGL 376
DB 442 EVIYQFVGLKSSMGYCGAPDLTLRD-----TAQFVRITGASLVESHPHGV 488

RESULT 24
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:27:41 ; Search time 32.37 Seconds
(without alignments)
1317.650 Million cell updates/sec

Title: US-09-853-918-30
Perfect score: 384
Sequence: 1 MADYLSIGGTGYVPEDGLTA.....MSAQIRGGVHGLSHYEKRLY 384

Scoring table: Oligo
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 11073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	146	38.0	604	22	ABG22269 Novel human diagno
2	66	17.2	66	22	ABG22265 Novel human diagno
3	55	14.3	55	22	AA75199 Human colon cancer
4	31	8.1	514	11	AA05432 Human IMPDH. Hom
5	31	8.1	514	11	AA05431 Chinese hamster IM
6	24	6.2	217	21	AA05491 Lung cancer associ
7	24	6.2	430	22	ABG23731 Novel human diagno
8	23	6.0	185	21	AA058731 Breast and ovarian
9	23	6.0	215	22	ABG22268 Novel human diagno
10	23	6.0	287	22	ABG07490 Novel human diagno
11	23	6.0	537	22	ABB58547 Drosophila melanog

12	23	6.0	537	22	ABB65768 Drosophila melanog
13	22	5.7	161	21	AA03970 Human secreted pro
14	21	5.5	371	20	AA08965 A. gossypii inosin
15	20	5.2	155	22	ABG22266 Novel human diagno
16	18	4.7	156	22	ABG22267 Novel human diagno
17	14	3.6	95	22	AA04552 Human polypeptide
18	14	3.6	151	20	AA08964 A. gossypii inosin
19	13	3.4	403	22	AA070679 S cerevisiae apopt
20	11	2.9	133	21	AA072702 Zea mays protein f
21	11	2.9	140	21	AA072701 Zea mays protein f
22	11	2.9	152	21	AA072700 Zea mays protein f
23	11	2.9	435	21	AA030890 Arabidopsis thalia
24	11	2.9	436	21	AA031110 Arabidopsis thalia
25	11	2.9	443	21	AA030889 Arabidopsis thalia
26	11	2.9	444	21	AA031109 Arabidopsis thalia
27	11	2.9	502	21	AA030888 Arabidopsis thalia
28	11	2.9	503	21	AA031108 Arabidopsis thalia
29	10	2.6	436	21	AA030890 Arabidopsis thalia
30	10	2.6	444	21	AA030990 Arabidopsis thalia
31	10	2.6	503	21	AA030989 Arabidopsis thalia
32	9	2.3	178	22	AA080108 Corynebacterium gl
33	9	2.3	489	21	AA097820 Pseudomonas sp. WF
34	9	2.3	506	22	AA090418 C glutamicum prote
35	9	2.3	506	22	AA080106 Corynebacterium gl
36	8	2.1	24	15	AA089189 GPR adrenergic rec
37	8	2.1	24	15	AA050808 G-protein coupled
38	8	2.1	24	17	AA02740 G-protein coupled
39	8	2.1	86	20	AA035259 Chlamydia pneumoni
40	8	2.1	139	21	AA031650 Arabidopsis thalia
41	8	2.1	143	21	AA031297 Arabidopsis thalia
42	8	2.1	143	21	AA031977 Arabidopsis thalia
43	8	2.1	158	20	AA041224 P. vulgaris YC43-P
44	8	2.1	164	21	AA031649 Arabidopsis thalia
45	8	2.1	174	21	AA031976 Arabidopsis thalia
46	8	2.1	177	21	AA031296 Arabidopsis thalia
47	8	2.1	181	21	AA036279 Human secreted pro
48	8	2.1	199	21	AA031295 Arabidopsis thalia
49	8	2.1	264	22	AB018250 Novel human diagno
50	8	2.1	307	22	AA040893 Propionibacterium
51	8	2.1	308	21	AA090005 Arabidopsis thalia
52	8	2.1	308	21	AA090002 Human gene 65-enco
53	8	2.1	325	22	AA035218 Enterococcus faeca
54	8	2.1	325	22	AA035950 Helicobacter pylor
55	8	2.1	327	22	AA033399 Enterococcus faeca
56	8	2.1	328	22	AA037668 Streptococcus pneu
57	8	2.1	348	21	AA090004 Arabidopsis thalia
58	8	2.1	348	21	AA037828 Arabidopsis thalia
59	8	2.1	349	21	AA031216 Arabidopsis thalia
60	8	2.1	362	21	AA031215 Arabidopsis thalia
61	8	2.1	367	21	AA090003 Arabidopsis thalia
62	8	2.1	367	21	AA037827 Arabidopsis thalia
63	8	2.1	368	21	AA031214 Arabidopsis thalia
64	8	2.1	386	21	AA037826 Arabidopsis thalia
65	8	2.1	473	21	AA042135 Human ORFX ORF1899
66	8	2.1	479	21	AA029656 Human membrane-ass
67	8	2.1	479	22	AA097000 Oesophagus cancer
68	8	2.1	481	19	AA011109 H. pylori ORF hp8e
69	8	2.1	481	19	AA098634 Murine zalpha30 po
70	8	2.1	700	22	AA000956 HII binding site c
71	7	1.8	7	22	AA045273 HII binding site c
72	7	1.8	7	22	AA045278 HII binding site c
73	7	1.8	7	22	AA045283 A metalloprotease
74	7	1.8	32	20	AA068536 NlpD repeat sequen
75	7	1.8	44	20	AA014005 Propionibacterium
76	7	1.8	57	22	AA074995 Human haematologic
77	7	1.8	60	22	AA080321 Propionibacterium
78	7	1.8	61	22	AA048738 Propionibacterium
79	7	1.8	62	22	AA055029 Propionibacterium
80	7	1.8	65	22	AA055029 Human immune/haema
81	7	1.8	67	22	AA062708 Arabidopsis thalia
82	7	1.8	71	21	AA024493 Arabidopsis thalia
83	7	1.8	71	21	AA038103 Arabidopsis thalia
84	7	1.8	72	22	AA070019 Mammalian CD4 IL-1

85 7 1.8 77 21 AAG24492 Arabidopsis thalia
 86 7 1.8 78 21 AAG38102 Arabidopsis thalia
 87 7 1.8 115 22 AAG91827 C glutamicum prote
 88 7 1.8 126 20 AAV12621 Human 5' EST seque
 89 7 1.8 129 21 AAG17469 Arabidopsis thalia
 90 7 1.8 135 21 AAG17468 Arabidopsis thalia
 91 7 1.8 139 21 AAG17467 Arabidopsis thalia
 92 7 1.8 142 21 AAG24491 Arabidopsis thalia
 93 7 1.8 143 21 AAG38101 Arabidopsis thalia
 94 7 1.8 148 21 AAG05976 Arabidopsis thalia
 95 7 1.8 149 22 AAM80713 Human haematologic
 96 7 1.8 153 22 AAM80008 Corynebacterium gl
 97 7 1.8 155 22 AAM81278 Human haematologic
 98 7 1.8 157 22 AAG89983 C glutamicum prote
 99 7 1.8 158 22 AAB80107 Corynebacterium gl
 100 7 1.8 165 20 AAY50044 Rhodobacter sphaer

ALIGNMENTS

RESULT 1
 ABG22269
 ID ABG22269 standard; Protein: 604 AA.
 XX
 AC ABG22269;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22260.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS86456.
 XX

New isolated polynucleotide and encoded polypeptides, useful in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits and to assess
 biodiversity -

Claim 20; SEQ ID No 52628; 103pp; English.

The invention relates to isolated polynucleotide (I) and
 polypeptide (II) sequences. (I) is useful as hybridisation probes,
 polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 and gene mapping, and in recombinant production of (II). The
 polynucleotides are also used in diagnostics as expressed sequence tags
 for identifying expressed genes. (I) is useful in gene therapy techniques
 to restore normal activity of (II) or to treat disease states involving
 (II). (II) is useful for generating antibodies against it, detecting or
 quantitating a polypeptide in tissue, as molecular weight markers and as
 a food supplement. (II) and its binding partners are useful in medical
 imaging of sites expressing (II). (I) and (II) are useful for treating
 disorders involving aberrant protein expression or biological activity.
 The polypeptide and polynucleotide sequences have applications in
 diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 604 AA;

Query Match 38.0%; Score 146; DB 22; Length 604;
 Best Local Similarity 100.0%; Pred. No. 3.6e-136;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 AEYARFGVPILADGGIQTGVHVVKALALGASTVMGMSLLAATTEAPGEYFFSDGVRLKK 280
 |||||
 Db 441 aeyarrfvpiladggigtvghvkvkaiagastvmgmsllaateapgeyffsdgvrllk 500
 |||||
 QY 281 YRGMGSLDAMEKSSSKRYFSEGDVKVIAQGVSGSIQDKSGIQKFPVPLIAGIQHGCQD 340
 |||||
 Db 501 yrgmsldameksssqkryfsegdvkkiagvsgsiqdkgsiqkfvpyliagiqhgccq 560
 |||||
 QY 341 IGARSLSVLRSMYSGELAFKRTMS 366
 |||||
 Db 561 igarslsvlrsmymysgelkfkrtms 586

RESULT 2
 ABG22265
 ID ABG22265 standard; Protein: 66 AA.
 XX
 AC ABG22265;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22256.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS86452.
 XX

New isolated polynucleotide and encoded polypeptides, useful in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits and to assess
 biodiversity -

Claim 20; SEQ ID No 52624; 103pp; English.

The invention relates to isolated polynucleotide (I) and
 polypeptide (II) sequences. (I) is useful as hybridisation probes,
 polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 and gene mapping, and in recombinant production of (II). The
 polynucleotides are also used in diagnostics as expressed sequence tags
 for identifying expressed genes. (I) is useful in gene therapy techniques
 to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 66 AA;

Query Match 17.2%; Score 66; DB 22; Length 66;
 Best Local Similarity 100.0%; Pred. No. 1.4e-57;
 Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 DKGSTQKFPVYLIAGTQHGCDIGARSLVLRSMYSGLKFEKRTMSAQIEGGVHGLHS 378

Db 1 dkgsiqkrtvpyliagiqhgcqdigarslvlrsmysgelkfekrtsaqieggvghlgs 60

QY 379 YEKRLY 384

|||||

Db 61 yekrly 66

RESULT 3

AAG75199

ID AAG75199 standard; Protein; 55 AA.

XX AC AAG75199;

XX DT 03-SEP-2001 (first entry)

XX DE Human colon cancer antigen protein SEQ ID NO:5963.

XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;

XX KW colorectal carcinoma; chromosome 7.

XX OS Homo sapiens.

XX PN WO200122920-A2.

XX PD 05-APR-2001.

XX PF 28-SEP-2000; 2000WO-US26524.

XX PR 29-SEP-1999; 98US-0157137.

XX PR 03-NOV-1999; 99US-0163280.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;

XX PI WPI; 2001-235357/24.

XX DR N-PSDB; AAH34604.

XX XX

PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 PS Claim 11; Page 7468-7469; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P

CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patients own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAB77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 55 AA;

Query Match 14.3%; Score 55; DB 22; Length 55;
 Best Local Similarity 100.0%; Pred. No. 9.8e-47;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 LIAGTQHGCDIGARSLVLRSMYSGLKFEKRTMSAQIEGGVHGLHSYEKRLY 384

Db 1 liagiqhgcqdigarslvlrsmysgelkfekrtsaqieggvghlshyekrly 55

RESULT 4

AAR05432

ID AAR05432 standard; protein; 514 AA.

XX AC AAR05432;

XX DT 31-AUG-1990 (first entry)

XX DE Human IMPDH.

XX KW Inosine 5'-mono-phosphate dehydrogenase; hepatomas;

XX KW guanosine monophosphate.

XX OS Homo sapiens.

XX PN WO9001545-A.

XX PD 22-FEB-1990.

XX PF 02-AUG-1989; 89WO-0000344.

XX PR 12-AUG-1988; 88US-0232302.

XX PA (ARCH-) ARCH. DEV. CORP.

XX PI Collart FR, Huberman E;

XX DR WPI; 1990-083504/11.

XX DR P-PSDB; AAR05432.

XX XX

PT DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -
 PT used to detect high levels of enzyme activity of tumour cells,
 PT esp. hepatomas, and to produce guanosine monophosphate.
 XX Claim 8; Fig 1; 51pp; English.

XX A 35 aa segment corresponds to deduced aa residues 336-370 in
 CC both the human and Chinese hamster proteins.
 CC See also AAQ03541.

XX Sequence 514 AA;

Query Match 8.1%; Score 31; DB 11; Length 514;

Best Local Similarity 100.0%; Pred. No. 5.5e-22;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
Db 375 kalgastvmgslllaatteapgeyffsdg 405

RESULT 5
AAR05431
ID AAR05431 standard; protein; 514 AA.
XX AAR05431;
XX 31-AUG-1990 (first entry)
XXR Chinese hamster IMPDH.
DE
XX Inosine 5'-mono-phosphate dehydrogenase; hepatomas;
KW guanosine monophosphate.
XX Cricetulus sp.
OS WO9001545-A.
PN 22-FEB-1990.
PD
XX 02-AUG-1989; 89WO-0000344.
PF 12-AUG-1988; 88US-0232302.
PR (ARCH-) ARCH. DEV. CORP.
XX Collart FR, Huberman E;
PI WPI; 1990-083504/11.
DR N-PSDB; AAQ03541.
XX DNA encoding eukaryotic inosine 5'-mono-phosphate dehydrogenase -
PT used to detect high levels of enzyme activity of tumour cells,
PT esp. hepatomas, and to produce guanosine monophosphate.
XX Claim 8; Fig 2; 51pp; English.
PS A 35 aa segment corresponds to deduced aa residues 336-370 in
CC both the human and Chinese hamster proteins.
CC See also AAQ03540.
XX Sequence 514 AA;

Query Match 8.1%; Score 31; DB 11; Length 514;
Best Local Similarity 100.0%; Pred. No. 5.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
Db 375 kalgastvmgslllaatteapgeyffsdg 405

RESULT 6
AAB58491
ID AAB58491 standard; protein; 217 AA.
XX AAB58491;
XX 14-MAR-2001 (first entry)
DE Lung cancer associated polypeptide sequence SEQ ID 829.
XX Human; lung cancer associated protein; neuroprotective; cytostatic;
KW cardioactive; immunomodulatory; muscular active; vulnerary;
KW gastrointestinal; nephrotropic; antiinfective; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease.
XX

OS Homo sapiens.
PN WO200055180-A2.
XX 21-SEP-2000.
PD
XX 08-MAR-2000; 2000WO-US05918.
PF 12-MAR-1999; 99US-0124270.
PR (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX Ruben SM;
XX WPI; 2000-587514/55.
DR N-PSDB; AAF18367.
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer -
XX Claim 11; Page 1370-1371; 1425pp; English.
PS Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
XX associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC antagonists may have neuroprotective; cytostatic; cardioactive;
CC immunomodulatory; muscular active general; vulnerary; gastrointestinal
CC general; nephrotropic; antiinfective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the
CC protein or polynucleotide sequences. The lung cancer associated
CC polynucleotide sequences may be used for detection of lung cancer,
CC chromosome identification, as chromosome markers, and for numerous other
CC diagnostic or research purposes. The proteins may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders. The proteins may also be used in the treatment of wounds and
CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
CC peptide AAB58549 are used in the course of the invention for the
CC identification and characterisation of the polynucleotide and protein
CC sequences.
XX Sequence 217 AA;

Query Match 6.2%; Score 24; DB 21; Length 217;
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 86 GGIGFIHNNCTPEFQANEVRKVK 109
Db 50 ggigfihnnctpefqanevrkvvk 73

RESULT 7
ABG23731
ID ABG23731 standard; Protein; 430 AA.
XX AC ABG23731;
XX 18-FEB-2002 (first entry)
DT Novel human diagnostic protein #23722.
DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
OS WO200175067-A2.
PN 11-OCT-2001.
PD

XX 30-MAR-2001; 2001WO-US08631.
 XX PF
 XX 31-MAR-2000; 2000US-0540217.
 XX PR
 XX 23-AUG-2000; 2000US-0649167.
 XX PR
 XX (HYSE-) HYSEQ INC.
 XX PA
 XX Drmanac RT, Liu C, Tang YT;
 XX PI
 XX WPI: 2001-639362/73.
 XX DR
 XX N-PSDB; AAS87918.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits and to assess
 XX biodiversity -
 XX
 XX Claim 20; SEQ ID No 54090; 103pp; English.
 XX PS
 XX The invention relates to isolated polynucleotide (I) and
 XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
 XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 XX and gene mapping, and in recombinant production of (II). The
 XX polynucleotides are also used in diagnostics as expressed sequence tags
 XX for identifying expressed genes. (I) is useful in gene therapy techniques
 XX to restore normal activity of (II) or to treat disease states involving
 XX (II). (II) is useful for generating antibodies against it, detecting or
 XX quantitating a polypeptide in tissue, as molecular weight markers and as
 XX a food supplement. (II) and its binding partners are useful in medical
 XX imaging of sites expressing (II). (I) and (II) are useful for treating
 XX disorders involving aberrant protein expression or biological activity.
 XX The polypeptide and polynucleotide sequences have applications in
 XX diagnostics, forensics, gene mapping, identification of mutations
 XX responsible for genetic disorders or other traits to assess biodiversity
 XX and to produce other types of data and products dependent on DNA and
 XX amino acid sequences. ABG00010-ABG30377 represent novel human
 XX diagnostic amino acid sequences of the invention.
 XX Note: The sequence data for this patent did not appear in the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 430 AA;
 XX
 XX Query Match 6.2%; Score 24; DB 22; Length 430;
 XX Best Local Similarity 100.0%; Pred. No. 4.2e-15;
 XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 MADYLISSGTYGYPEDGLTAQQLF 24
 XX |
 XX Db 9 madyliisgtygypedgltaqqlf 32
 XX
 XX RESULT 8
 XX AAB58731
 XX ID AAB58731 standard; Protein; 185 AA.
 XX AC AAB58731;
 XX XX
 XX DT 27-MAR-2001 (first entry)
 XX XX
 XX DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 439.
 XX XX
 XX KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 XX KW neotropic; neuroprotective; antiviral; antitumor; hepatotropic;
 XX KW antidiabetic; antiinflammatory; antitumor; antitumor; antitumor;
 XX KW antitumor; antitumor; antitumor; antitumor; antitumor;
 XX KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 XX KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 XX KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 XX KW cardiovascular disorder; wound healing; neurological disease.
 XX XX

OS Homo sapiens.
 XX XX
 XX PN WO2000055173-A1.
 XX XX
 XX PD 21-SEP-2000.
 XX XX
 XX PF 08-MAR-2000; 2000WO-US05881.
 XX XX
 XX PR 12-MAR-1999; 99US-0124270.
 XX PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PA
 XX Rosen CA, Ruben SM;
 XX PI
 XX WPI: 2000-611515/58.
 XX DR
 XX N-PSDB; AAF21634.
 XX XX
 XX New human breast and ovarian cancer associated gene sequences and the
 XX polypeptides encoded by these genes, useful in the prevention,
 XX treatment and diagnosis of cancer, immune disorders, cardiovascular
 XX disorders and neurological diseases -
 XX
 XX Claim 11; Page 865-866; 1299pp; English.
 XX PS
 XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 XX proteins AAB58711 - AAB59128. The DNA and protein sequences are
 XX associated with breast and ovarian cancer. Included in the invention are
 XX sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 XX isolation and characterisation of the DNA and protein sequences of the
 XX invention. The breast and ovarian cancer associated DNA, protein, agonist
 XX or antagonist sequences exhibit cytostatic; immunosuppressive;
 XX neotropic; neuroprotective; antiviral; antitumor; antitumor;
 XX antidiabetic; antiinflammatory; antitumor; antitumor; antitumor;
 XX antibacterial; antifungal; antiparasitic; antitumor; antitumor;
 XX polynucleotide and protein sequences are used in the diagnosis of cancer,
 XX particularly breast and ovarian cancer. The nucleic acid sequences,
 XX proteins, agonists and antagonists may also be used in the diagnosis,
 XX prevention and treatment of immune disorders e.g. Addison's disease,
 XX allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 XX diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 XX arthritis and ulcerative colitis; cardiovascular disorders such as
 XX myocardial ischaemia; wound healing; neurological diseases such as
 XX cerebral anoxia and epilepsy; and infectious diseases.
 XX
 XX Sequence 185 AA;
 XX
 XX Query Match 6.0%; Score 23; DB 21; Length 185;
 XX Best Local Similarity 100.0%; Pred. No. 1.9e-14;
 XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 167 LQVIGSNVTVTAQAQKLNLDAGVD 189
 XX |
 XX Db 98 lqvignvntaaqaknldagvd 120
 XX
 XX RESULT 9
 XX ABG22268
 XX ID ABG22268 standard; Protein; 215 AA.
 XX XX
 XX AC ABG22268;
 XX XX
 XX DT 18-FEB-2002 (first entry)
 XX XX
 XX DE Novel human diagnostic protein #22259.
 XX XX
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX XX
 XX OS Homo sapiens.
 XX XX
 XX PN WO200175067-A2.
 XX XX

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PD 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX N-PSDB; AAS86455.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID No 52627; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 215 AA;

Query Match 6.0%; Score 23; DB 22; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AIAMALMGIGFIHHNCTPEFQA 101
Db 4 aiamaimgigfihhncptefqa 26

RESULT 10
ABG07490
ID ABG07490 standard; Protein; 287 AA.
XX
XX ABG07490;
AC
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX Novel human diagnostic protein #7481.
DE
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensics;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX
XX WO200175067-A2.
PN
XX
XX 11-OCT-2001.
PD

XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX N-PSDB; AAS71677.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID No 37849; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 287 AA;

Query Match 6.0%; Score 23; DB 22; Length 287;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AIAMALMGIGFIHHNCTPEFQA 101
Db 76 aiamaimgigfihhncptefqa 98

RESULT 11
ABB58547
ID ABB58547 standard; Protein; 537 AA.
XX
XX ABB58547;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 2433.
DE
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD

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PF 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 XX N-PSDB; ABL02650.
 DR
 DR New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PT
 PS Disclosure; SEQ ID NO 2433; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 537 AA;

Query Match 6.0%; Score 23; DB 22; Length 537;
 Best Local Similarity 100.0%; Pred. No. 5.1e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 EAPGEYFFSDGVRLKKYRGMGSL 287
 |||||||
 Db 414 eapgeyffsdgvrlkkymgmsl 436

RESULT 12
 ABB65768
 ID ABB65768 standard; Protein; 537 AA.
 XX
 AC ABB65768;

XX 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 24096.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL09871.
 XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 XX Disclosure; SEQ ID NO 24096; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 537 AA;

Query Match 6.0%; Score 23; DB 22; Length 537;
 Best Local Similarity 100.0%; Pred. No. 5.1e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 EAPGEYFFSDGVRLKKYRGMGSL 287
 |||||||
 Db 414 eapgeyffsdgvrlkkymgmsl 436

RESULT 13
 AAG03970
 ID AAG03970 standard; Protein; 161 AA.
 XX
 AC AAG03970;

XX 06-OCT-2000 (first entry)
 XX Human secreted protein, SEQ ID NO: 8051.
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX Homo sapiens.
 OS
 XX EP1033401-A2.
 PN
 PD 06-SEP-2000.
 XX
 XX 21-FEB-2000; 2000EP-0200610.
 PF
 XX 26-FEB-1999; 99US-0122487.
 PR
 XX (GEST) GENSET.
 PA
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 PI WPI; 2000-500381/45.
 XX N-PSDB; AAC03976.
 DR
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 13; SEQ ID 8051; 71pp + CD-ROM; English.
 XX

The present sequence is a polypeptide encoded by one of a large number
 of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 were prepared from total human RNAs or polyA+ RNAs derived from 30
 different tissues. EST sequences usually correspond mainly to the 3'
 untranslated region (UTR) of the mRNA because they are often obtained
 from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 isolating cDNA sequences derived from the 5' ends of mRNAs and even in

CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.
XX
SQ Sequence 161 AA;

Query Match 5.7%; Score 22; DB 21; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GGIGFIHHNCTPFOANEVRKV 107
|||||
DB 86 ggigfihhnmctpefqanevrkv 107

RESULT 14
AAY08965
ID AAY08965 standard; Protein; 371 AA.

XX AC AAY08965;

XX DT 19-AUG-1999 (first entry)

DE DE A. gossypii inosine-monophosphate dehydrogenase protein fragment 2.

XX KW Purine biosynthesis; phosphoribosylpyrophosphate synthetase; KPR1; KPR2;
KW glutamine-phosphoribosylpyrophosphate amidotransferase; ADE4; GUA1;
KW IMP-dehydrogenase; GUA1; GMP-synthetase; GUA2; PRPP synthetase; mouth;
KW riboflavin; vitamin B2; treatment; inflammation; throat; mucosal layer;
KW skin disorder.

XX OS Ashbya gossypii.

XX PI EP927761-A2.

XX PD 07-JUL-1999.

XX PF 08-DEC-1998; 98EP-0123331.

XX PR 23-DEC-1997; 97DE-1057755.

XX PA (BADI) BASF AG.

XX PI Hoeffken HW, Jimenez A, Pompejus M, Revuelta Doval JL;
PI Santos Garcia MA, Seuilberger H;

XX DR WPI; 1999-373465/32.

XX DR N-PSDB; AAX78081.

XX PT Ashbya gossypii purine biosynthesis enzymes and related genes for
PT production of riboflavin

XX PS Claim 13; Page 33-34; 48pp; German.

XX CC This invention describes novel enzymes involved in purine biosynthesis
CC in Ashbya gossypii. The enzymes described in the invention include
CC Phosphoribosylpyrophosphate (PRPP) synthetases KPR1 and KPR2
CC glutamine-phosphoribosylpyrophosphate amidotransferase (ADE4)
CC IMP-dehydrogenase (GUA1) and a GMP-synthetase (GUA2). The nucleic acid
CC sequences encoding the enzymes involved in purine biosynthesis are used
CC to genetically modify microorganisms, for the production of riboflavin.
CC Riboflavin, also known as vitamin B2, is essential in humans and animals
CC and is used to treat inflammation of the mouth and throat mucosal layer
CC as well as inflammation in skin disorders. This sequence represents a
CC fragment of the inosine-monophosphate dehydrogenase protein encoded by
CC the GUA1 gene represented in AAX78081.

XX SQ Sequence 371 AA;

Query Match 5.5%; Score 21; DB 20; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVNACGRPGGTAVY 218
|||||
DB 180 gsicitqevnmacgrpggtavy 200

RESULT 15
ABG22266
ID ABG22266 standard; Protein; 155 AA.

XX AC ABG22266;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #22257.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSEQ-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS86453.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

XX PS Claim 20; SEQ ID No 52625; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: the sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 155 AA;

Query Match 5.2%; Score 20; DB 22; Length 155;
 Best Local Similarity 100.0%; Pred. No. 1.5e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 GLTYNDFLLPGFIDFIAD 48
 Db 23 gityndflllpfidiade 42

RESULT 16

ABG222267
 ID ABG222267 standard; Protein; 156 AA.

XX AC ABG222267;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #22259.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS86454.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX PS Claim 20; SEQ ID No 52626; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.

XX CC Note: the sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 156 AA;

Query Match 4.7%; Score 18; DB 22; Length 156;

Best Local Similarity 100.0%; Pred. No. 1.5e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 TLKTPLISSPMDTVTEAD 77
 Db 3 tlktpLISSpmdtvtead 20

RESULT 17

AAO04552
 ID AAO04552 standard; Protein; 95 AA.

XX AC AAO04552;

XX DT 06-NOV-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 18444.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

XX PN WO200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US04927.

XX PR 28-FEB-2000; 2000US-0515126.

XX PR 18-MAY-2000; 2000US-0577409.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-514838/56.

XX DR N-PSDB; AAI84483.

XX PT Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders -

XX PS Claim 20; SEQ ID NO 18444; 1399pp + Sequence Listing; English.

XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.

XX CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 95 AA;

Query Match 3.6%; Score 14; DB 22; Length 95;

Best Local Similarity 100.0%; Pred. No. 8.9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GGIGFIHNCNCTPEF 99

Db 61 ggigfihhncnctpef 74

RESULT 18
AAV08964
ID AAV08964 standard; Protein; 151 AA.
XX
AC AAV08964;
XX
DT 19-AUG-1999 (first entry)
XX
DE A. gossypii inosine-monophosphate dehydrogenase protein fragment 1.
XX
KW Purine biosynthesis; phosphoribosylpyrophosphate synthetase; KPR1; KPR2;
KW glutamine-phosphoribosylpyrophosphate amidotransferase; ADE4; GUA1;
KW IMP-dehydrogenase; GUA1; GMP-synthetase; GUA2; PRPP synthetase; mouth;
KW riboflavin; vitamin B2; treatment; inflammation; throat; mucosal layer;
KW skin disorder.
XX
OS Ashbya gossypii.
XX
PN EP927761-A2.
XX
PD 07-JUL-1999.
XX
PF 08-DEC-1998; 98EP-0123331.
XX
PR 23-DEC-1997; 97DE-1057755.
XX
PA (BADI) BASF AG.
XX
PI Hoeffken HW, Jimenez A, Pompejus M, Revuelta Doval JL;
PI Santos Garcia MA, Seulberger H;
XX
DR N-PSDB; AAX78081.
XX
PT Ashbya gossypii purine biosynthesis enzymes and related genes for
PT production of riboflavin
XX
PS Claim 13; Page 32-33; 48pp; German.
XX
CC This invention describes novel enzymes involved in purine biosynthesis
CC in Ashbya gossypii. The enzymes described in the invention include
CC Phosphoribosylpyrophosphate (PRPP) synthetases KPR1 and KPR2
CC glutamine-phosphoribosylpyrophosphate amidotransferase (ADE4)
CC IMP-dehydrogenase (GUA1) and a GMP-synthetase (GUA2). The nucleic acid
CC sequences encoding the enzymes involved in purine biosynthesis are used
CC to genetically modify microorganisms, for the production of riboflavin.
CC Riboflavin, also known as vitamin B2, is essential in humans and animals
CC and is used to treat inflammation of the mouth and throat mucosal layer
CC as well as inflammation in skin disorders. This sequence represents a
CC fragment of the inosine-monophosphate dehydrogenase protein encoded by
CC the GUA1 gene represented in AAX78081.
XX
SQ Sequence 151 AA;

Query Match 3.6%; Score 14; DB 20; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTEADMAI 80
Db 73 sspmdtvtreadmai 86
|||||

RESULT 19
AAG70679
ID AAG70679 standard; Protein; 403 AA.
XX
AC AAG70679;
XX
DT 27-JUL-2001 (first entry)
XX

DE S cerevisiae apoptosis associated protein YAR073W.
XX
KW Yeast; fungus; apoptosis; infection; proliferative disease;
KW vaccine; autoimmune disease; ischaemia; neurodegeneration.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200102550-A2.
XX
PD 11-JAN-2001.
XX
PF 03-JUL-2000; 2000WO-BE00077.
XX
PR 01-JUL-1999; 99EP-0870141.
XX
PA (JANC) JANSSEN PHARM NV.
XX
PI Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;
PI Nellissen BJM, Reekmans RJ;
XX
DR WPI; 2001-367042/38.
DR N-PSDB; AAH29715.
XX
PT Yeast and fungal nucleic acids encoding proteins involved in a pathway
PT leading to programmed cell death, useful for treating proliferative
PT disorders, yeast and fungal infections, or for preventing apoptosis in
PT certain diseases.
XX
PS Claim 1; Fig 1; 218pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC number of apoptosis associated proteins from the yeast Saccharomyces
CC cerevisiae and the fungus Candida albicans. These can be used to identify
CC treatments for fungal and yeast infections, for proliferative diseases
CC and for apoptosis related diseases such as autoimmune diseases, ischaemia
CC and neurodegeneration. The present sequence is one of the S. cerevisiae
CC proteins of the invention.
XX
SQ Sequence 403 AA;

Query Match 3.4%; Score 13; DB 22; Length 403;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 VMACGRPQGTAVY 218
Db 340 vmacgrpqqgtavy 352
|||||

RESULT 20
AAG27202
ID AAG27202 standard; Protein; 133 AA.
XX
AC AAG27202;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 31947.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR	13-OCT-1999;	99US-0159294.	PR	28-APR-1999;	99US-0131449.
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KW	KW	termination sequence; corn.			
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Query Match 2.98; Score 11; DB 21; Length 140;
Best Local Similarity 100.0%; Pred. NO. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 17-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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Query Match 2.9%; Score 11; DB 21; Length 435;
Best Local Similarity 100.0%; Pred. No. 0.035; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

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RESULT 24
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XX AC
XX DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
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XX PN EP1033405-A2.
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XX XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX XX
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XX XX
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
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Query Match 2.9% Score 11; DB 21; Length 502;
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Db 306 agvdglrvmg 316

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DT 18-OCT-2000 (first entry)
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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XX DT 17-OCT-2000 (first entry)

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XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX KW termination sequence.

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PR	24-JUN-1999;	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	PR	10-SEP-1999;	99US-0153070.

PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159369.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159638.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.
Query Match 2.6%; Score 10; DB 21; Length 436; Best Local Similarity 100.0%; Pred. No. 0.35; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	241	gvdglrvmg 250
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DE	Arabidopsis thaliana protein fragment SEQ ID NO: 23384.	
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KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
XX	XX	termination sequence.
OS	Arabidopsis thaliana.	
PN	EP1033405-A2.	
XX	XX	
PD	06-SEP-2000.	
XX	XX	

PR 09-JUL-1999; 99US-0142820.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
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PR 13-SEP-1999; 99US-0153758.
PR 13-SEP-1999; 99US-0154018.
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PR 29-SEP-1999; 99US-0156596.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.6%; Score 10; DB 21; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.35;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GVDGLRVGMG 196

Db 249 gvdglrvgmg 258

RESULT 31

AAG20989

ID AAG20989 standard; Protein; 503 AA.

XX AAG20989;

AC AAG20989;

XX 17-OCT-2000 (first entry)

DT

DE Arabidopsis thaliana protein fragment SEQ ID NO: 23383.

XX

Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

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PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

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PR 01-APR-1999; 99US-0127462.
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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
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 PR 28-OCT-1999; 99US-0161992.
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Query Match 2.6%; Score 10; DB 21; Length 503;

Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GVDGLRVGMG 196

Db 308 gvdglrvgm 317

RESULT 32

AAB80108
 ID AAB80108 standard; Protein; 178 AA.

XX AC AAB80108;

XX 30-APR-2001 (first entry)

XX Corynebacterium glutamicum MP protein sequence SEQ ID NO:950.

XX Corynebacterium glutamicum; metabolic pathway protein; MP protein;
 KW fine chemical production; microorganism; organic acid; nucleoside;
 KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
 KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
 KW carbohydrate; aromatic compound; cofactor; polyketide; enzyme.

XX OS Corynebacterium glutamicum.

XX WO200100843-A2.

XX 04-JAN-2001.

XX 23-JUN-2000; 2000WO-IB00923.

XX 25-JUN-1999; 99US-0141031.
 PR 01-JUL-1999; 99DE-1030476.
 PR 02-JUL-1999; 99US-0142101.
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 PR 03-SEP-1999; 99DE-1042124.
 PR 03-SEP-1999; 99DE-1042129.
 PR 09-MAR-2000; 2000US-0187970.

(BADI) BASF AG.

Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;

WPI; 2001-137957/14.

N-PSDB; AAF72227.

Nucleic acids from Corynebacterium glutamicum encoding metabolic
 pathway proteins, useful for producing fine chemicals in
 microorganisms, including organic acids, nonproteinogenic amino acids,
 and purine and pyrimidine bases -

Claim 20; Page 1455; 1737pp; English.

AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic
 pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum
 MP nucleic acids are useful for the production of fine chemicals
 in microorganisms, including organic acids, nonproteinogenic amino
 acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,
 saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
 compounds, vitamins, cofactors, polyketides and enzymes.

Sequence 178 AA;

Query Match 2.3%; Score 9; DB 22; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPITADGG 236
Db 16 gvpitadgg 24
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RESULT 33
AAY97820
ID AAY97820 standard; Protein; 489-AA.
XX AC AAY97820;
XX XX
XX 29-AUG-2000 (first entry)
XX DE Pseudomonas sp. WF505 ORF6-3 protein, SEQ ID NO:5.
XX KW Benzothioophene oxidase; bto gene cluster; desulphurisation; crude oil;
XX KW decontamination.
XX OS Pseudomonas sp. WF505.
XX PN JP2000093180-A.
XX PD 04-APR-2000.
XX PF 28-SEP-1998; 98JP-0272744.
XX PR 28-SEP-1998; 98JP-0272744.
XX PA (TOFU) TONEN CORP.
XX XX
XX WPI; 2000-378972/33.
DR N-PSDB; AAA38391.
XX XX
XX New proteins useful for desulfurization of crude oil have ability to
XX control expression of benzothioophene oxidase group -
XX
XX Example 1; Page 19-20; 43pp; Japanese.
XX
XX The invention relates to proteins encoded by the benzothioophene oxidase
XX (bto) gene cluster from Pseudomonas sp. WF505, specifically the protein
XX which controls expression of the gene cluster (AAY97827), the
XX benzothioophene oxidase (bto) enzyme itself (AAY97825) and a
XX benzothioophene oxidase co-enzyme (AAY97824), which controls
XX benzothioophene activity via redox regulation. These enzymes are
XX respectively encoded by the bto gene cluster open reading frames ORF2-16
XX (AAA38398), ORF4-9 (AAA38396) and ORF6-7 (AAA38395). The invention also
XX encompasses genetic constructs and vectors comprising the genes encoding
XX these proteins, hosts containing such constructs and the recombinant
XX production of the enzymes. Pseudomonas sp. WF505 benzothioophene oxidase,
XX benzothioophene oxidase co-enzyme and bto gene cluster regulator are
XX useful in the desulfurization of crude oil and petroleum products, and
XX for the clarification of soil and waste water contaminated by organic
XX sulphur compounds. Sequences AAY97819-Y97829 represent the proteins
XX encoded by the genes of the Pseudomonas sp. WF505 benzothioophene oxidase
XX gene cluster.
XX
XX Sequence 489 AA;

Query Match 2.3%; Score 9; DB 21; Length 489;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 GASTVMNGS 258
Db 352 gastvmngs 360
|||||

RESULT 34
AAG90418
ID AAG90418 standard; Protein; 506-AA.
XX AC AAG90418;
XX XX
XX 26-SEP-2001 (first entry)
XX DE C glutamicum protein fragment SEQ ID NO: 4172.
XX KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
XX KW organic acid synthesis.
XX OS Corynebacterium glutamicum.
XX PN EP1108790-A2.
XX PD 20-JUN-2001.
XX PF 18-DEC-2000; 2000EP-0127688.
XX PR 16-DEC-1999; 99JP-0377484.
XX PR 07-APR-2000; 2000JP-0159162.
XX PR 03-AUG-2000; 2000JP-0280988.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.
XX PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
XX PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
XX DR WPI; 2001-376931/40.
XX DR N-PSDB; AAH65637.
XX PT Novel polynucleotides derived from Coryneform bacteria, for identifying
XX PT mutation point of a gene, measuring expression of a gene, analysing
XX PT expression profile or pattern of a gene and identifying homologous gene
XX
XX Claim 17; SEQ ID NO: 4172; 246pp + Sequence Listing; English.
XX PS The present invention provides a number of nucleotide and protein
XX sequences from the Coryneform bacterium Corynebacterium glutamicum. These
XX are useful for identifying the mutation point of a gene derived from a
XX mutant of coryneform bacterium, measuring expression amount and
XX analysing the expression profile or expressing pattern of a gene derived
XX from Coryneform bacterium, and identifying a homologue of a gene derived
XX from coryneform bacterium. Coryneform bacteria are useful for producing
XX amino acids, nucleic acids, vitamins, saccharides and organic acids,
XX particularly L-lysine. The present sequence is a protein described
XX in the exemplification of the invention.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from the
XX CC European Patent Office.
XX
XX Sequence 506 AA;

Query Match 2.3%; Score 9; DB 22; Length 506;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPITADGG 236
Db 344 gvpitadgg 352
|||||

RESULT 35
AAB80106
ID AAB80106 standard; Protein; 506-AA.
XX AC AAB80106;
XX XX
XX 30-APR-2001 (first entry)

XX DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:946.
XX DE
XX KW fine chemical production; microorganism; organic acid; nucleoside;
KW KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
KW KW lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
XX KW carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
OS
XX OS Corynebacterium glutamicum.
XX PN WO200100843-A2.
XX PN
XX PD 04-JAN-2001.
XX PF
XX PF 23-JUN-2000; 2000WO-IB00923.
XX PR
XX PR 25-JUN-1999; 99US-0141031.
PR PR 01-JUL-1999; 99DE-1030476.
PR PR 02-JUL-1999; 99US-0142101.
PR PR 08-JUL-1999; 99DE-1031415.
PR PR 08-JUL-1999; 99DE-1031418.
PR PR 08-JUL-1999; 99DE-1031419.
PR PR 08-JUL-1999; 99DE-1031420.
PR PR 08-JUL-1999; 99DE-1031424.
PR PR 08-JUL-1999; 99DE-1031428.
PR PR 08-JUL-1999; 99DE-1031434.
PR PR 08-JUL-1999; 99DE-1031435.
PR PR 08-JUL-1999; 99DE-1031443.
PR PR 08-JUL-1999; 99DE-1031453.
PR PR 08-JUL-1999; 99DE-1031457.
PR PR 08-JUL-1999; 99DE-1031465.
PR PR 08-JUL-1999; 99DE-1031478.
PR PR 08-JUL-1999; 99DE-1031510.
PR PR 08-JUL-1999; 99DE-1031541.
PR PR 08-JUL-1999; 99DE-1031573.
PR PR 08-JUL-1999; 99DE-1031592.
PR PR 08-JUL-1999; 99DE-1031632.
PR PR 08-JUL-1999; 99DE-1031634.
PR PR 08-JUL-1999; 99DE-1031636.
PR PR 08-JUL-1999; 99DE-1032125.
PR PR 08-JUL-1999; 99DE-1032126.
PR PR 08-JUL-1999; 99DE-1032130.
PR PR 08-JUL-1999; 99DE-1032186.
PR PR 08-JUL-1999; 99DE-1032206.
PR PR 08-JUL-1999; 99DE-1032227.
PR PR 08-JUL-1999; 99DE-1032228.
PR PR 08-JUL-1999; 99DE-1032229.
PR PR 08-JUL-1999; 99DE-1032230.
PR PR 14-JUL-1999; 99DE-1032922.
PR PR 14-JUL-1999; 99DE-1032926.
PR PR 14-JUL-1999; 99DE-1032928.
PR PR 14-JUL-1999; 99DE-1033004.
PR PR 14-JUL-1999; 99DE-1033005.
PR PR 14-JUL-1999; 99DE-1033006.
PR PR 12-AUG-1999; 99US-0148613.
PR PR 27-AUG-1999; 99DE-1040764.
PR PR 27-AUG-1999; 99DE-1040765.
PR PR 27-AUG-1999; 99DE-1040766.
PR PR 27-AUG-1999; 99DE-1040832.
PR PR 31-AUG-1999; 99DE-1041378.
PR PR 31-AUG-1999; 99DE-1041379.
PR PR 31-AUG-1999; 99DE-1041380.
PR PR 31-AUG-1999; 99DE-1041394.
PR PR 31-AUG-1999; 99DE-1041396.
PR PR 03-SEP-1999; 99DE-1042076.
PR PR 03-SEP-1999; 99DE-1042077.
PR PR 03-SEP-1999; 99DE-1042079.
PR PR 03-SEP-1999; 99DE-1042086.
PR PR 03-SEP-1999; 99DE-1042087.
PR PR 03-SEP-1999; 99DE-1042088.
PR PR 03-SEP-1999; 99DE-1042095.
PR PR 03-SEP-1999; 99DE-1042124.

PR 03-SEP-1999; 99DE-1042129.
PR 09-MAR-2000; 2000US-0187970.
XX
XX PA (BADI) BASF AG.
XX PI Pompejus M, Kroegeer B, Schroeder H, Zelder O, Haberhauer G;
XX WPI; 2001-137957/14.
DR N-PSDB; AAF72225.
XX
XX Nucleic acids from Corynebacterium glutamicum encoding metabolic
PT pathway proteins, useful for producing fine chemicals in
PT microorganisms, including organic acids, nonproteinogenic amino acids,
PT and purine and pyrimidine bases -
XX
XX Claim 20; Page 1451-1452; 1737pp; English.
XX
XX AAF71753 to AAF72330 encode the Corynebacterium glutamicum metabolic
CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum
CC MP nucleic acids are useful for the production of fine chemicals
CC in microorganisms, including organic acids, nonproteinogenic amino
CC acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,
CC saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
CC compounds, vitamins, cofactors, polyketides and enzymes.
XX
SQ Sequence 506 AA;

Query Match 2.3%; Score 9; DB 22; Length 506;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPPIADGG 236
Db 344 gvpiaagg 352
|||||

RESULT 36
AAR89189
ID AAR89189 standard; peptide; 24 AA.
XX
XX AC AAR89189;
XX
XX DT 07-JUN-1996 (first entry)
XX
XX DE GPR adrenergic receptor TM consensus sequence #10.
XX
XX G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;
KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
KW rhodopsin; opsin; odorant; cytomegalovirus; serotonergic.
XX
XX OS Synthetic.
XX
XX WO9405695-A1.
XX
XX PD 17-MAR-1994.
XX
XX PF 09-SEP-1993; 93WO-US08528.
XX
XX PR 10-SEP-1992; 92US-0943236.
XX
XX (UYN) UNIV NEW YORK STATE.
XX
XX PI Murphy RB, Schuster DI;
XX
XX WPI; 1994-101120/12.
DR
PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for
PT binding GPR ligands or modulating GPR binding
XX
XX Claim 8; Page 136; 160pp; English.

CC The sequence of a polypeptide, based on the consensus sequence from
 CC transmembrane domains of adrenergic receptors, used in a G-protein
 CC coupled receptor ligand binding assay. The assay can be used to
 CC identify fragments pref. transmembrane fragments, from G-protein coupled
 CC receptor (GPR) proteins (see AAR48686-R48758 for examples) which retain
 CC biological activity such as binding a GPR ligand or modulating GPR ligand
 CC binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and
 CC AAR89189-R89195 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 XX

SQ Sequence 24 AA;

Query Match 2.1%; Score 8; DB 15; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 IGGNVVTA 177
 Db 15 iggnvvta 22
 |||||

RESULT 37

AAR50808
 ID AAR50808 standard; peptide; 24 AA.

AC AAR50808;

XX 17-MAY-1996 (first entry)

DE G-protein coupled serotonergic receptor consensus sequence #4.

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;
 KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;
 KW rhodopsin; opsin; odorant; cytomagalovirus; serotonergic.

OS Synthetic.

PN WO9405695-A1.

XX 17-MAR-1994.

PF 09-SEP-1993; 93WO-US08528.

XX 10-SEP-1992; 92US-0943236.

PR (UUNY) UNIV NEW YORK STATE.

PA Murphy RB, Schuster DI;

XX WPI; 1994-101120/12.

XX Polypeptides of G-coupled receptor proteins (GPRs) - useful for
 PT binding GPR ligands or modulating GPR binding

XX Disclosure; Page 34; 160pp; English.

XX Peptides AAR50808-14 are peptides based on serotonergic receptor (5-HT)
 CC transmembrane domain consensus sequences, used in a G-protein coupled
 CC receptor ligand binding assay. The assay can be used to identify
 CC fragments pref. transmembrane fragments, from G-protein coupled receptor
 CC (GPR) proteins (see AAR48686-R48758 for examples) which retain
 CC biological activity such as binding a GPR ligand or modulating GPR ligand
 CC binding to a GPR (see AAR48759-R48758, AAR50569-R50807 and
 CC AAR89189-R89195 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 XX

SQ Sequence 24 AA;

Query Match 2.1%; Score 8; DB 15; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 IGGNVVTA 177
 Db 15 iggnvvta 22
 |||||

RESULT 38

AAW02740
 ID AAW02740 standard; peptide; 24 AA.

XX AC AAW02740;

XX 13-NOV-1996 (first entry)

DE G-protein coupled serotonergic (5-HT) receptor consensus sequence #4.

KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
 KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
 KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
 KW odorant; cytomagalovirus; serotonergic.

OS Synthetic.

PN US5508384-A.

XX 16-APR-1996.

XX 10-SEP-1992; 92US-0943236.

XX 09-SEP-1993; 93US-0118270.

XX 10-SEP-1992; 92US-0943236.

PA (UUNY) UNIV NEW YORK STATE.

XX Murphy RB, Schuster DI;

XX WPI; 1996-208785/21.

XX New dopamine receptor peptide - useful as antipsychotic agent, e.g.
 PT for treating schizophrenia

XX Disclosure; Column 27; 184pp; English.

XX The sequence of a polypeptide, based on the serotonergic receptor (5-HT)
 CC transmembrane domain consensus sequences, used in a G-protein coupled
 CC receptor ligand binding assay. The assay can be used to identify
 CC fragments pref. transmembrane fragments, from G-protein coupled receptor
 CC (GPR) proteins (AAW02657-W02730) which retain biological activity such
 CC as binding a GPR ligand or modulating GPR ligand binding to a GPR (see
 CC AAW02747-W02999 for examples of polypeptide fragments). The polypeptide
 CC fragments can be used in compositions for treating subjects suffering
 CC from a pathology related to a GPR abnormality e.g. a psychotic disorder
 CC such as schizophrenia.
 XX

SQ Sequence 24 AA;

Query Match 2.1%; Score 8; DB 17; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 IGGNVVTA 177
 Db 15 iggnvvta 22
 |||||

RESULT 39

AAV35259

```
ID AAY35259 standard; Protein; 86 AA.
XX
AC AAY35259;
XX
XX
DT 13-SEP-1999 (first entry)
XX
XX Chlamydia pneumoniae ribosomal polypeptide.
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope.
XX
XX Chlamydia pneumoniae.
OS
XX WO9927105-A2.
PN
XX 03-JUN-1999.
PD
XX 20-NOV-1998; 98WO-IB01890.
PF
XX 04-NOV-1998; 98US-0107078.
PR
XX 21-NOV-1997; 97FR-0014673.
XX
PA (GEST ) GENSET.
XX
XX Griffais R;
PI
XX WPI; 1999-357842/30.
DR
XX
XX Genome sequence of Chlamydia pneumoniae
PT
XX Page 1092-1093; Disclosure; 1912pp; English.
PS
XX AAY34584-Y35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAX91950) of Chlamydia pneumoniae.
CC C. pneumoniae causes respiratory disease such as pneumonia and
CC bronchitis and is thought to be a contributing factor in heart
CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in
CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae.
XX
SQ Sequence 86 AA;

Query Match 2.1%; Score 8; DB 20; Length 86;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 SEGDKVKI 309
    |||||
Db 57 segdkvki 64

RESULT 40
AAG51650
ID AAG51650 standard; Protein; 139 AA.
XX
AC AAG51650;
XX
XX 18-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana protein fragment SEQ ID NO: 65575.
DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
OS
XX
```

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PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
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PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144632.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.

PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 2.1%; Score 8; DB 21; Length 139;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 DGLTAQQL 23
| | | | | | | |
Db 120 dgltaqql 127

Search completed: September 26, 2002, 08:32:00
Job time: 259 sec

ALIGNMENTS

```
RESULT 1
US-08-925-230-7
; Sequence 7, Application US/08925230
; Patent No. 6147194
; GENERAL INFORMATION:
; APPLICANT: Collart, Frank
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,230
; FILING DATE: September 8, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,665,583
; FILING DATE: 12-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 7:
; LENGTH: 514 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-925-230-7

Query Match      8.1%; Score 31; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
DB 375 KALALGASTVMGSLLAATTEAPGEYFFSDG 405
|||||
|||||

RESULT 2
US-08-925-230-8
; Sequence 8, Application US/08925230
; Patent No. 6147194
; GENERAL INFORMATION:
; APPLICANT: Collart, Frank
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO IMPDH
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/925,230
; FILING DATE: September 8, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 5,665,583
; FILING DATE: 12-AUG-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mark B.
; REGISTRATION NUMBER: 37,259
; REFERENCE/DOCKET NUMBER: ARCD:274
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 514 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-925-230-8

Query Match      8.1%; Score 31; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
DB 375 KALALGASTVMGSLLAATTEAPGEYFFSDG 405
|||||
|||||
```

```
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,230
FILING DATE: September 8, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 5,665,583
FILING DATE: 12-AUG-1988
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:274
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-925-230-8

Query Match      8.1%; Score 31; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGSLLAATTEAPGEYFFSDG 275
DB 375 KALALGASTVMGSLLAATTEAPGEYFFSDG 405
|||||
|||||

RESULT 3
US-08-118-270-89
; Sequence 89, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-89

Query Match 2.1%; Score 8; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 IGGNVVTA 177
Db 15 IGGNVVTA 22
|||||

RESULT 4

PCT-US93-08528-89
Sequence 89, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-89

Query Match 2.1%; Score 8; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 IGGNVVTA 177
Db 15 IGGNVVTA 22
|||||

RESULT 5

US-09-053-197A-19
Sequence 19, Application US/09053197A
Patent No. 6022952
GENERAL INFORMATION:
APPLICANT: Weiner, Joel H.
APPLICANT: Turner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
TITLE OF INVENTION: SECRETION
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,197A
FILING DATE: 01-APR-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MacKnight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: UALB-03293

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 158 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-09-053-197A-19

Query Match 2.1%; Score 8; DB 3; Length 158;

Best Local Similarity 100.0%; Pred. No. 3.8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 APGEYFFS 273
|||||

Db 49 APGEYFFS 56
|||||

RESULT 6

US-09-085-761A-19
Sequence 19, Application US/09085761A
Patent No. 6335178
GENERAL INFORMATION:
APPLICANT: Weiner, Joel H.
APPLICANT: Turner, Raymond J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTEIN
TITLE OF INVENTION: SECRETION
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/085,761A
; FILING DATE: 28-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: UALB-03356
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-085-761A-19

Query Match 2.1%; Score 8; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 APGEYFFS 273
| | | | |
Db 49 APGEYFFS 56

RESULT 7
US-09-082-090-5
; Sequence 5, Application US/09082090
; Patent No. 6090583
; GENERAL INFORMATION:
; APPLICANT: CLINKENBEARD, HELEN
; APPLICANT: SOUTHAN, CHRISTOPHER
; APPLICANT: BURGESS, NICOLA
; TITLE OF INVENTION: No. 6090583el compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,090
; FILING DATE: 20-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711310.4
; FILING DATE: 30-MAY-1997
; APPLICATION NUMBER: GB 9803690.8
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F.
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-30332
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846189
; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-082-090-5

Query Match 1.8%; Score 7; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 SLSVLRS 351
| | | | |
Db 17 SLSVLRS 23

RESULT 8
US-08-253-823-1
; Sequence 1, Application US/08253823
; Patent No. 5541094
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: GLYCOLATE OXIDASE PRODUCTION
; NUMBER OF SEQUENCES: 1
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM
; OPERATING SYSTEM: MICROSOFT WINDOWS V3.0
; SOFTWARE: MICROSOFT WORD V2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,823
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/085,488
; FILING DATE: JULY 1, 1993
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-253-823-1

Query Match 1.8%; Score 7; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGA 251
| | | | |
Db 296 KALALGA 302

RESULT 9
US-08-290-508-3
; Sequence 3, Application US/08290508
; Patent No. 5693490
; GENERAL INFORMATION:
; APPLICANT: PAYNE, MARK S.
; APPLICANT: ANTON, DAVID L.
; APPLICANT: DICOSIMO, ROBERT
; APPLICANT: GAVAGAN, JOHN E.
; TITLE OF INVENTION: Production of glycolate oxidase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS
; ADDRESSEE: AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE


```

; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH 1.0 MB
; COMPUTER: MACINTOSH
; OPERATING SYSTEM: MACINTOSH SYSTEM, 6.0
; SOFTWARE: MICROSOFT WORD, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290.508
; FILING DATE: 15-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/025.495
; FILING DATE: 03-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: GALLEGOS, R. THOMAS
; REGISTRATION NUMBER: 32,692
; REFERENCE/DOCKET NUMBER: CR-9271
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-7342
; TELEFAX: 302-892-7949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-290-508-3

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```

Query Match 1.8%; Score 7; DB 1; Length 369;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 245 KALALGA 251
Db 296 KALALGA 302

```

```

RESULT 10
US-08-606-144-1
; Sequence 1, Application US/08606144
; Patent No. 5834262
; GENERAL INFORMATION:
; APPLICANT: DAVID LEROY ANTON
; APPLICANT: ROBERT DICOSIMO
; TITLE OF INVENTION: OXIDATION OF GLYCOLIC ACID TO
; TITLE OF INVENTION: GLYOXYLIC ACID USING A
; TITLE OF INVENTION: MICROBIAL CELL TRANSFORMANT
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E.JI.DJUIPONTJDEINEMOURS
; ADDRESSEE: AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH 2.0 MB
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS, 3.1
; SOFTWARE: MICROSOFT WORD VERSION 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/606.144
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/817.165
; FILING DATE: JANUARY 6, 1992
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: GREGORY, THEODORE C.
; REGISTRATION NUMBER: 25,243
; REFERENCE/DOCKET NUMBER: CH-2087-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4925
; TELEFAX: 302-773-0184
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-606-144-1

```

```

Query Match 1.8%; Score 7; DB 2; Length 369;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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QY 245 KALALGA 251
Db 296 KALALGA 302

```

```

RESULT 11
PCT-US94-02174-3
; Sequence 3, Application PC/TUS9402174
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Production of
; TITLE OF INVENTION: glycolate oxidase IN
; TITLE OF INVENTION: methylotrophic yeast
; NUMBER OF SEQUENCES: 3
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH 1.0 MB
; COMPUTER: MACINTOSH
; OPERATING SYSTEM: MACINTOSH SYSTEM, 6.0
; SOFTWARE: MICROSOFT WORD, 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02174
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US94-02174-3

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```

Query Match 1.8%; Score 7; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 245 KALALGA 251
Db 296 KALALGA 302

```

```

RESULT 12
US-08-191-866D-21
; Sequence 21, Application US/08191866D
; Patent No. 5783195
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D
; APPLICANT: Macdonald, Richard D.
; TITLE OF INVENTION: Recombinant Infectious Bovine
; TITLE OF INVENTION: Rhinotracheitis Virus S-IBR-052 And Uses Thereof
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191,866D
FILING DATE: 4 February 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-191-866D-21

Query Match 1.8%; Score 7; DB 1; Length 441;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 LLCGAAV 120
Db 16 LLCGAAV 22

RESULT 13
US-08-185-949B-21
Sequence 21, Application US/08185949B
Patent No. 5874279
GENERAL INFORMATION:
APPLICANT: Mark D. Cochran
APPLICANT: Richard D. Macdonald
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotracheitis Virus
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,949B
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0525
INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-185-949B-21

Query Match 1.8%; Score 7; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 LLCGAAV 120
Db 16 LLCGAAV 22

RESULT 14
US-08-843-417-10
Sequence 10, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-843-417-10

Query Match 1.8%; Score 7; DB 4; Length 1956;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 SLSVLRS 351
Db 751 SLSVLRS 757

RESULT 15
US-09-036-987A-6
; Sequence 6, Application US/09036987A
; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Treadway, Patti J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences LLC Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,987A
; FILING DATE: 09-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R.
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5588 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-036-987A-6

Query Match 1.8%; Score 7; DB 4; Length 5588;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LISGGTG 11
Db 1407 LISGGTG 1413

RESULT 16
US-09-370-700-6
; Sequence 6, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700

; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5588
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-6

Query Match 1.8%; Score 7; DB 4; Length 5588;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LISGGTG 11
Db 1407 LISGGTG 1413

RESULT 17
US-08-484-044-8
; Sequence 8, Application US/08484044
; Patent No. 5552282
; GENERAL INFORMATION:
; APPLICANT: Caskey, C. T.
; APPLICANT: Fu, Ying-Hui
; APPLICANT: Friedman, David L.
; APPLICANT: Pizzuti, Antonio
; APPLICANT: Fenwick, Raymond G.
; TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,044
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/019,940
; FILING DATE: 19-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5443
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; TELEX: 762829
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-044-8

Query Match 1.6%; Score 6; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 EDGLTA 20
|||||
Db 3 EDGLTA 8

RESULT 18

US-09-140-149-11
; Sequence 11, Application US/09140149
; Patent No. 6117680
; APPLICANT: Natesan, Sridaran
; APPLICANT: Gilman, Michael Z
; TITLE OF INVENTION: No. 6117680el Compositions and Methods for Regulation of
; FILE REFERENCE: 363C
; CURRENT APPLICATION NUMBER: US/09/140,149
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 08/918,401
; EARLIER FILING DATE: 1997-08-26
; EARLIER APPLICATION NUMBER: 08/920,610
; EARLIER FILING DATE: 1997-08-27
; EARLIER APPLICATION NUMBER: 09/126,009
; EARLIER FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: PC1/US97/15219
; EARLIER FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-09-140-149-11

Query Match 1.6%; Score 6; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 ALALGA 251
|||||
Db 2 ALALGA 7

RESULT 19

US-08-399-696-109
; Sequence 109, Application US/08399696
; Patent No. 5756669
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: p53-BINDING POLYPEPTIDES AND
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME
; NUMBER OF SEQUENCES: 126
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/399,696
; FILING DATE: 02-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156,671
; FILING DATE: 22-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15522-000710
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-399-696-109

Query Match 1.6%; Score 6; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 178 AQAKNL 183
|||||
Db 1 AQAKNL 6

RESULT 20

US-08-112-208C-14
; Sequence 14, Application US/08112208C
; Patent No. 5691179
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,208C
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-112-208C-14

Query Match 1.6%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 FFSDGV 276
|||||
Db 4 FFSDGV 9

RESULT 21

US-08-248-819A-16

; Sequence 16, Application US/08248819A
; Patent No. 5700638
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248.819A
; FILING DATE: 25-NAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112.208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000610
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-248-819A-16

Query Match 1.6%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 FFSDGV 276
Db 4 FFSDGV 9

RESULT 22
US-08-337-646A-34
; Sequence 34, Application US/08337646A
; Patent No. 5856171
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/337.646A

; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248.819
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112.208
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000620
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-337-646A-34

Query Match 1.6%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 271 FFSDGV 276
Db 4 FFSDGV 9

RESULT 23
US-08-856-531-14
; Sequence 14, Application US/08856531
; Patent No. 5942490
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856.531
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..23
; OTHER INFORMATION: /note= "Peptide fragment from
; OTHER INFORMATION: Figure 14A"
US-08-856-531-14

Query Match 1.6%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 FFSDGV 276
|
|
|
|
|
Db 4 FFSDGV 9

RESULT 24
US-08-856-034-14
; Sequence 14, Application US/08856034
; Patent No. 5955595
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howell & Haferkamp, L.C.
; STREET: 7733 Forsyth Blvd., Suite 1400
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63105

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/856,034
; FILING DATE:

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, Donald R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 976175
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..23
; OTHER INFORMATION: /note= "Peptide fragment from
; OTHER INFORMATION: Figure 14A"
US-08-856-034-14

Query Match 1.6%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 FFSDGV 276
|
|
|
|
|
Db 4 FFSDGV 9

RESULT 25
US-08-808-277A-16

; Sequence 16, Application US/08808277A
; Patent No. 5998374
; GENERAL INFORMATION:
; APPLICANT: LEHRER, ROBERT I.
; APPLICANT: LEE, IN-HEE
; APPLICANT: ZHAO, CHENGQUAN
; TITLE OF INVENTION: CLAVASPIRINS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,277A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 220002057300
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:

; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5998374e
US-08-808-277A-16

Query Match 1.6%; Score 6; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 VGHVVK 245
|
|
|
|
|
Db 12 VGHVVK 17

RESULT 26
US-08-927-326-34
; Sequence 34, Application US/08927326
; Patent No. 6184202
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: CELL DEATH REGULATORS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/927,326
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/337,646
;; FILING DATE: 10-NOV-1994
;; APPLICATION NUMBER: US 08/248,819
;; FILING DATE: 25-MAY-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/112,208
;; FILING DATE: 26-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Smith, William M
;; REGISTRATION NUMBER: 30,223
;; REFERENCE/DOCKET NUMBER: 15726A-000620
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 34:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-08-927-326-34

Query Match 1.6%; Score 6; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 FFSQGV 276
Db 4 FFSQGV 9

RESULT 27
US-08-628-291-14
;; Sequence 14, Application US/08628291
;; Patent No. 5801031
;; GENERAL INFORMATION:
;; APPLICANT: GALIVAN, JOHN H.
;; APPLICANT: RYAN, THOMAS J.
;; APPLICANT: YAO, RONG
;; APPLICANT: NIMEC, ZENIA
;; TITLE OF INVENTION: GAMMA GLUTAMYL HYDROLASE
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
;; COUNTRY: USA
;; ZIP: 14603
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/628,291
;; FILING DATE:
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: TIMIAN, SUSAN J.
;; REGISTRATION NUMBER: 34,103
;; REFERENCE/DOCKET NUMBER: 20894/150
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 716-263-1636
;; TELEFAX: 716-263-1600
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-628-291-14

Query Match 1.6%; Score 6; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 LLCGAA 119
Db 14 LLCGAA 19

RESULT 28
US-09-128-722-14
;; Sequence 14, Application US/09128722
;; Patent No. 5962235
;; GENERAL INFORMATION:
;; APPLICANT: Galivan, John H
;; APPLICANT: Ryan, Thomas J
;; APPLICANT: Yao, Rong
;; APPLICANT: Nimec, Zenia
;; TITLE OF INVENTION: Gamma Glutamyl Hydrolase
;; NUMBER OF SEQUENCES: 16
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Jaekle Fleischmann & Mugel, LLP
;; STREET: 39 State Street
;; CITY: Rochester
;; STATE: New York
;; COUNTRY: US
;; ZIP: 14614-1310
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/128,722
;; FILING DATE: 04-AUG-1998
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/628,291
;; FILING DATE: 05-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Braham, Susan J
;; REGISTRATION NUMBER: 34,103
;; REFERENCE/DOCKET NUMBER: 87681.98R196
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 716-262-3640
;; TELEFAX: 716-262-4133
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-128-722-14

Query Match 1.6%; Score 6; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 LLCGAA 119
Db 14 LLCGAA 19

RESULT 29

US-08-975-080-28
; Sequence 28, Application US/08975080
; Patent No. 6245523
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,080
; FILING DATE: 20-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELEPHONE: 202-467-7176
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-975-080-28

Query Match 1.6%; Score 6; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 EGDVKV 308
Db 4 EGDVKV 9

RESULT 30
US-08-975-080-29
; Sequence 29, Application US/08975080
; Patent No. 6245523
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

US-08-975-080-32
; Sequence 32, Application US/08975080
; Patent No. 6245523
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,080
; FILING DATE: 20-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-975-080-29

Query Match 1.6%; Score 6; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 EGDVKV 308
Db 4 EGDVKV 9

RESULT 31
US-08-975-080-32
; Sequence 32, Application US/08975080
; Patent No. 6245523
; GENERAL INFORMATION:
; APPLICANT: Altieri, Dario C.
; TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
; TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,080
; FILING DATE: 20-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,435
; FILING DATE: 20-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044574-5022-01-WO
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-975-080-32

Query Match 1.6%; Score 6; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 EGDVKV 308
|||||
Db 4 EGDVKV 9

RESULT 32

US-08-630-916A-82
; Sequence 82, Application US/08630916A
; Patent No. 6011137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-916A-82

Query Match 1.6%; Score 6; DB 3; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 EDGLTA 20
|||||
Db 8 EDGLTA 13

RESULT 33

US-08-511-485-24
; Sequence 24, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen

; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-24

Query Match 1.6%; Score 6; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 EGDVKV 308
|||||
Db 30 EGDVKV 35

RESULT 34

US-08-511-485-25
; Sequence 25, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-25

Query Match 1.6%; Score 6; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 EGDVKV 308
Db 30 EGDVKV 35

RESULT 35
US-08-487-031-17
Sequence 17, Application US/08487031
Patent No. 5977306
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
APPLICANT: Mika-Grieve, Marcia
APPLICANT: Tripp, Cynthia A.
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,031
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-34-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-031-17

Query Match 1.6%; Score 6; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 356 GELKFE 361
Db 59 GELKFE 64

RESULT 36
US-08-473-034-17
Sequence 17, Application US/08473034
Patent No. 6114142
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
APPLICANT: Mika-Grieve, Marcia
APPLICANT: Tripp, Cynthia A.
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,034
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-473-034-17

Query Match 1.6%; Score 6; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 GELKFE 361
Db 59 GELKFE 64

RESULT 37
US-08-487-031-7
Sequence 7, Application US/08487031
Patent No. 5977306
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
APPLICANT: Mika-Grieve, Marcia
APPLICANT: Tripp, Cynthia A.
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,031
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-34-1
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-031-7

Query Match 1.6%; Score 6; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 356 GELKFE 361
Db 59 GELKFE 64

RESULT 38
US-08-473-034-7
Sequence 7, Application US/08473034
Patent No. 6114142
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Frank, Glenn R.
APPLICANT: Mika-Grieve, Marcia
APPLICANT: Tripp, Cynthia A.
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH P39
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,034
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-34
TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 72 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-473-034-7

Query Match 1.6%; Score 6; DB 3; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 356 GELKFE 361
Db 59 GELKFE 64

RESULT 39
US-08-355-888A-11
Sequence 11, Application US/08355888A
Patent No. 5763211
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: HU-BI.219, A NOVEL HUMAN HEMATOPOIETIN
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/355,888A
FILING DATE: 14-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7225-078
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 73 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-355-888A-11

Query Match 1.6%; Score 6; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 209 CGRPQG 214
Db 31 CGRPQG 36

RESULT 40
US-08-693-697-11
; Sequence 11, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-693-697-11

Query Match 1.6%; Score 6; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 209 CGRPQG 214
|
Db 31 CGRPQG 36

Search completed: September 26, 2002, 08:32:21
Job time: 240 sec

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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:29:26 ; Search time 20.9 seconds
(without alignments)
1765.469 Million cell updates/sec

Title: US-09-853-918-30

Perfect score: 384

Sequence: 1 MADYLISGCTGYVPEDGLTA.....MSAQIEGCVHGLHSYEKRLY 384

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271	70.6	514	1 A35566	IMP dehydrogenase
2	31	8.1	514	1 A31997	IMP dehydrogenase
3	31	8.1	514	1 B31997	IMP dehydrogenase
4	31	8.1	514	1 J70565	IMP dehydrogenase
5	23	6.0	537	1 S41064	IMP dehydrogenase
6	23	6.0	537	1 S59508	IMP dehydrogenase
7	21	5.5	523	1 S59402	IMP dehydrogenase
8	21	5.5	523	1 S48997	IMP dehydrogenase
9	21	5.5	524	1 S50890	IMP dehydrogenase
10	14	3.6	509	2 J7305	IMP dehydrogenase
11	14	3.6	514	1 A38668	IMP dehydrogenase
12	13	3.4	403	1 S53477	IMP dehydrogenase
13	13	3.4	499	1 T32709	IMP dehydrogenase
14	13	3.4	524	1 T40127	IMP dehydrogenase
15	11	2.9	502	2 F86298	IMP dehydrogenase
16	11	2.9	503	1 J64999	IMP dehydrogenase
17	10	2.6	485	2 D3652	inositol-monophosph
18	10	2.6	485	2 D97232	IMP dehydrogenase
19	10	2.6	742	2 H95270	probable kinase/es
20	9	2.3	444	1 D72631	probable IMP dehyd
21	9	2.3	482	2 C72264	IMP dehydrogenase
22	9	2.3	495	2 S34810	probable oxygenase
23	9	2.3	496	1 G64501	IMP dehydrogenase
24	9	2.3	512	1 A55407	IMP dehydrogenase
25	9	2.3	1035	1 GNFFG1	retrovirus-related
26	8	2.1	86	2 H72054	ribosomal protein
27	8	2.1	86	2 C86570	S17 ribosomal prot
28	8	2.1	157	1 S78078	IMP dehydrogenase-
29	8	2.1	206	2 AE0160	probable glutathio

30	2.1	208	2	C96948	deoxyphosphoglucon
31	2.1	254	2	S73185	hypothetical prote
32	2.1	283	2	T09388	(S)-2-hydroxy-acid
33	2.1	290	2	T07032	(S)-2-hydroxy-acid
34	2.1	302	2	H96792	unknown protein F1
35	2.1	325	1	A71887	probable GMP reduc
36	2.1	326	1	C70015	probable GMP reduc
37	2.1	327	1	F64626	probable GMP reduc
38	2.1	327	2	D97326	GMP reductase [imp
39	2.1	328	2	A95145	conserved hypothet
40	2.1	328	2	G98012	GMP reductase [imp
41	2.1	358	2	AC1610	hypothetical prote
42	2.1	364	2	C84221	hypothetical prote
43	2.1	367	2	T10242	(S)-2-hydroxy-acid
44	2.1	368	2	T04532	probable (S)-2-hyd
45	2.1	368	2	G85206	glycolate oxidase-
46	2.1	368	2	A71727	hypothetical prote
47	2.1	393	2	B44767	L-mandelate dehydr
48	2.1	481	1	E54623	IMP dehydrogenase
49	2.1	481	1	H71890	IMP dehydrogenase
50	2.1	490	1	H70473	IMP dehydrogenase
51	2.1	521	1	T17196	IMP dehydrogenase
52	2.1	594	2	A75379	peptide ABC transp
53	2.1	1009	2	S26840	retrovirus-related
54	2.1	1009	2	S64734	retrovirus-related
55	7	91	2	G70238	hypothetical prote
56	7	96	2	E81047	hypothetical prote
57	7	104	2	B84037	thioredoxin trxa [
58	7	114	2	C81829	hypothetical prote
59	7	117	2	F87136	very hypothetical
60	7	135	2	C82821	NADH dehydrogenase
61	7	140	2	C71804	flagellar basal-bo
62	7	149	2	T03477	potential phosphat
63	7	153	2	A27179	collagen alpha 1(I
64	7	159	2	F82766	translation initia
65	7	166	2	A75383	hypothetical prote
66	7	179	2	C97117	signal peptidase I
67	7	187	2	G83243	peptidyl-prolyl ci
68	7	188	2	S39829	probable membrane
69	7	217	2	T46225	alpha NAC-like pro
70	7	217	2	D71866	hypothetical prote
71	7	222	2	C75539	conserved hypothet
72	7	224	2	S51579	cystathionine gamm
73	7	246	1	C72109	IMP dehydrogenase
74	7	246	2	D86512	inosine 5'-monopho
75	7	250	2	T04496	hypothetical prote
76	7	255	2	D71404	hypothetical prote
77	7	264	2	A12112	hypothetical prote
78	7	282	2	S50454	hypothetical prote
79	7	282	2	F64316	hypothetical prote
80	7	289	2	S16557	hypothetical prote
81	7	289	2	S16556	hypothetical prote
82	7	293	2	T50940	DiLD protein [impo
83	7	294	2	C82643	daunorubicin C-13
84	7	297	1	A30586	B-cell surface ant
85	7	299	1	A70118	glycine betaine, L
86	7	301	2	S28708	hypothetical prote
87	7	306	2	F64381	dihydroorotate oxi
88	7	307	2	G70665	hypothetical prote
89	7	308	2	AH2625	fructokinase [impo
90	7	311	2	S71228	O-succinylhomoseri
91	7	311	2	A86640	hypothetical prote
92	7	313	2	G97407	fructokinase [impo
93	7	319	2	S30173	probable mercuric
94	7	322	2	T31849	hypothetical prote
95	7	327	2	C91118	hypothetical prote
96	7	327	2	B85963	hypothetical prote
97	7	328	2	A82180	chemotaxis protein
98	7	332	2	I40726	rep protein - Cory
99	7	333	2	T06865	hypothetical prote
100	7	334	2	T12072	ABC-type permease

ALIGNMENTS

RESULT 1	
A35566	
IMP dehydrogenase (EC 1.1.1.205) I - human	
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenas	
C:Species: Homo sapiens (man)	
C:Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 05-May-2000	
C:Accession: A35566	
R:Natsumeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.	
J. Biol. Chem. 265, 5292-5295, 1990	
A:Title: Two distinct cDNAs for human IMP dehydrogenase.	
A:Reference number: A35566; MUID:90203022	
A:Accession: A35566	
A:Molecule type: mRNA	
A:Residues: 1-514 <NAT>	
A:Cross-references: GB:J05272; NID:gl186393	
A:Note: the sequence in GenBank entry HUMIMPH, release 103, (PID:g307067) has 273-Phe, 2	
C:Comment: mRNA for IMP dehydrogenase I predominated in normal leukocytes, whereas that	
C:Genetics:	
A:Gene: GDB:IMPDH1; SWS22608	
A:Cross-references: GDB:128085; OMIM:146690	
A:Map position: 7q31.3-7q32	
C:Function:	
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule	
A:Pathway: purine nucleotide biosynthesis	
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology	
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn	
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDNH>	
F:117-168/Domain: CBS homology <CBS1>	
F:184-232/Domain: CBS homology <CBS2>	
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>	
F:331/Active site: Cys #status predicted	
Query Match 70.6%; Score 271; DB 1; Length 514;	
Best Local Similarity 100.0%; Pred. No. 4.3e-265;	
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 114	LLCGAAGTREDKRYDLTLQAGDVIVLDDSSQGSNVIQIAVMHYIKQKYPHLQVIGGN 173
Db 244	LLCGAAGTREDKRYDLTLQAGDVIVLDDSSQGSNVIQIAVMHYIKQKYPHLQVIGGN 303
QY 174	VVTTAAQAKNLIDAGVGLRGVGMCGSICITQEVNACGRPGQTAVYKVAEYARRFGVPPIA 233
Db 304	VVTTAAQAKNLIDAGVGLRGVGMCGSICITQEVNACGRPGQTAVYKVAEYARRFGVPPIA 363
QY 234	DGGIQTGVHVVKALALGASTVMMGSLLAATTEAPGEYFFSDGVRLKKYRGMGSLDAMEKS 293
Db 364	DGGIQTGVHVVKALALGASTVMMGSLLAATTEAPGEYFFSDGVRLKKYRGMGSLDAMEKS 423
QY 294	SSSQKRYFSEGDVKVTKAQVSGSIQDKSGIQKFPVYLIAGIQHCCODIGARSLSVLRSMM 353
Db 424	SSSQKRYFSEGDVKVTKAQVSGSIQDKSGIQKFPVYLIAGIQHCCODIGARSLSVLRSMM 483
QY 354	YSGELKFEKRTMSAQIEGGVHGLHSYEKRLY 384
Db 484	YSGELKFEKRTMSAQIEGGVHGLHSYEKRLY 514
RESULT 2	
A31997	
IMP dehydrogenase (EC 1.1.1.205) II - human	
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH) type II	
C:Species: Homo sapiens (man)	
C:Date: 21-May-1990 #sequence_revision 22-May-1998 #text_change 16-Jul-1999	
C:Accession: I52303; I54184; A92676; B35566; A31997; A94550	
R:Giesne, D.A.; Huberman, E.	
Biochem. Biophys. Res. Commun. 205, 537-544, 1994	
A:Title: Cloning and sequence of the human type II IMP dehydrogenase gene.	
A:Reference number: I52303; MUID:95091778	
A:Accession: I52303	

A:Status: translated from GB/EMBL/DBDJ	
A:Molecule type: DNA	
A:Residues: 1-514 <GLEI>	
A:Cross-references: GB:I33842; NID:g602457; PIDN:AAA67054.1; PID:g602458	
R:Glesne, D.A.; Collart, F.R.; Varkony, T.; Drabkin, H.; Huberman, E.	
Genomics 16, 274-277, 1993	
A:Title: Chromosomal localization and structure of the human type II IMP dehydrogenas	
A:Reference number: I54184; MUID:93252398	
A:Accession: I54184	
A:Status: preliminary; translated from GB/EMBL/DBDJ	
A:Molecule type: DNA	
A:Residues: 461-514 <GLE2>	
A:Cross-references: GB:I08114; NID:g292239; PIDN:AAA36113.1; PID:g292240	
R:Collart, F.R.; Huberman, E.	
J. Biol. Chem. 263, 15769-15772, 1988	
A:Title: Cloning and sequence analysis of the human and Chinese hamster inosine-5'-mo	
A:Reference number: A92676; MUID:89008491	
A:Accession: A92676	
A:Molecule type: mRNA	
A:Residues: 1-189,'RS',192-514 <COL>	
A:Cross-references: GB:J04208; NID:gl186391; PIDN:AAA36112.1; PID:g307066	
A:Note: submitted to the Protein Sequence Database, November 1989	
R:Natsumeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.	
J. Biol. Chem. 265, 5292-5295, 1990	
A:Title: Two distinct cDNAs for human IMP dehydrogenase.	
A:Reference number: A35566; MUID:90203022	
A:Accession: B35566	
A:Status: nucleic acid sequence not shown; not compared with conceptual translation	
A:Molecule type: mRNA	
A:Residues: 1-514 <NAT>	
C:Comment: mRNA for IMP dehydrogenase I (see PIR:A35566) predominated in normal leuko	
C:Genetics:	
A:Gene: GDB:IMPDH2	
A:Cross-references: GDB:128086; OMIM:146691	
A:Map position: 3p24.2-3p21.2	
A:Introns: 33/2; 49/3; 83/3; 108/3; 177/3; 207/1; 274/1; 304/1; 336/1; 432/2; 480/2;	
C:Function:	
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecu	
A:Pathway: purine nucleotide biosynthesis	
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo	
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis	
F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDNH>	
F:117-168/Domain: CBS homology <CBS1>	
F:184-232/Domain: CBS homology <CBS2>	
F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>	
F:331/Active site: Cys #status predicted	
Query Match 8.1%; Score 31; DB 1; Length 514;	
Best Local Similarity 100.0%; Pred. No. 8.9e-23;	
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 245	KALALGASTVMMGSLLAATTEAPGEYFFSDG 275
Db 375	KALALGASTVMMGSLLAATTEAPGEYFFSDG 405
RESULT 3	
B31997	
IMP dehydrogenase (EC 1.1.1.205) - Chinese hamster	
N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydroge	
C:Species: Crictetus griseus (Chinese hamster)	
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000	
A:Accession: B31997	
R:Collart, F.R.; Huberman, E.	
J. Biol. Chem. 263, 15769-15772, 1988	
A:Title: Cloning and sequence analysis of the human and Chinese hamster inosine-5'-mo	
A:Reference number: A92676; MUID:89008491	
A:Accession: B31997	
A:Molecule type: mRNA	
A:Residues: 1-514 <COL>	
A:Cross-references: GB:J04209; NID:gl91119; PIDN:AAA36993.1; PID:g304517	
C:Function:	

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of NADPH
 A:Pathway: purine nucleotide biosynthesis
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
 C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
 F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:117-168/Domain: CBS homology <CBS1>
 F:184-232/Domain: CBS homology <CBS2>
 F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:331/Active site: Cys #status predicted

Query Match 8.1%; Score 31; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 8.9e-23;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGMSLLAATTEAPGEYFFSDG 275

Db 375 KALALGASTVMGMSLLAATTEAPGEYFFSDG 405

RESULT 4

IMP dehydrogenase (EC 1.1.1.205) - mouse
 N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
 C:Accession: J0565; A34375; S42724
 R:Tiedeman, A.A.; Smith, J.M.
 Gene 97, 289-293, 1991

A:Title: Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase.

A:Reference number: J0565; MUID:91153661

A:Accession: J0565

A:Molecule type: mRNA

A:Residues: 1-514 <TIE>

A:Cross-references: GB:M33934; NID:g198393; PIDN:AAA39311.1; PID:g309413

R:Hodges, S.D.; Fung, E.; McKay, D.J.; Renaux, B.S.; Snyder, F.F.

J. Biol. Chem. 264, 18137-18141, 1989

A:Title: Increased activity, amount, and altered kinetic properties of IMP dehydrogenase

A:Reference number: A34375; MUID:90036890

A:Accession: A34375

A:Molecule type: protein

A:Residues: 125-134;182-194;289-290;439-449;456-457, 'L',459-464, 'S',466;475-478 <HOD>

R:Lightfoot, T.; Snyder, F.F.

Biochim. Biophys. Acta 1217, 156-162, 1994

A:Title: Gene amplification and dual point mutations of mouse IMP dehydrogenase associated

A:Reference number: S42724; MUID:94153991

A:Accession: S42724

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-332, 'I',334-350, 'Y',352-482, 'M',484-514 <LIG>

A:Cross-references: EMBL:M98333; NID:g425157; PIDN:AAA20181.1; PID:g425158

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1993

C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of NADPH

A:Pathway: purine nucleotide biosynthesis

C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology

C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

F:30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>

F:117-168/Domain: CBS homology <CBS1>

F:184-232/Domain: CBS homology <CBS2>

F:233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>

F:331/Active site: Cys #status predicted

Query Match 8.1%; Score 31; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 8.9e-23;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGMSLLAATTEAPGEYFFSDG 275

Db 375 KALALGASTVMGMSLLAATTEAPGEYFFSDG 405

RESULT 5

S41064

IMP dehydrogenase (EC 1.1.1.205) imph - fruit fly (Drosophila melanogaster)
 N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
 C:Species: Drosophila melanogaster
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
 C:Accession: S41064; S61482
 R:Sifri, C.D.; Willson, K.; Smolik, S.; Forte, M.; Ullman, B.
 Biochim. Biophys. Acta 1217, 103-106, 1994
 A:Title: Cloning and sequence analysis of a Drosophila melanogaster cDNA encoding IMP
 A:Reference number: S41064; MUID:94114565
 A:Accession: S41064
 A:Molecule type: mRNA
 A:Residues: 1-537 <SIF>

A:Cross-references: EMBL:L22608; NID:g348101; PIDN:AAA16839.1; PID:g348102
 R:Nash, D.; Hu, S.; Leonard, N.J.; Tiong, S.Y.K.; Phillips, D.
 Genome 37, 333-344, 1994

A:Title: The raspberry locus of Drosophila melanogaster includes an inosine monophosph

A:Reference number: S61482; MUID:94259281

A:Accession: S61482

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-537 <NAS>

C:Genetics:

A:Cross-references: FlyBase:FBgn0003204

A:Map position: 10

A:Introns: 55/2; 105/3; 323/1; 503/2

C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule

C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo

C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio

F:52-118/Domain: IMP dehydrogenase amino-terminal homology <IDHN>

F:139-189/Domain: CBS homology <CBS1>

F:203-251/Domain: CBS homology <CBS2>

F:252-499/Domain: IMP dehydrogenase catalytic homology <IDHC>

F:350/Active site: Cys #status predicted

Query Match 6.0%; Score 23; DB 1; Length 537;

Best Local Similarity 100.0%; Pred. No. 1.1e-14;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 EAPGEYFFSDGVRLKKYRGMSL 287

Db 414 EAPGEYFFSDGVRLKKYRGMSL 436

RESULT 6

S59508

IMP dehydrogenase (EC 1.1.1.205) ras - fruit fly (Drosophila sp.)
 N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine-5'-monophosphate dehydrogenase
 C:Species: Drosophila sp.
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 05-May-2000
 C:Accession: S59508

R:Slee, R.; Bownes, M.

Mol. Gen. Genet. 248, 755-766, 1995

A:Title: The raspberry locus encodes Drosophila inosine monophosphate dehydrogenase.

A:Reference number: S59508; MUID:96069715

A:Accession: S59508

A:Molecule type: mRNA

A:Residues: 1-537 <SLE>

A:Cross-references: GB:S80430; NID:gl245860; PIDN:AAB35628.1; PID:gl245861

C:Genetics:

A:Gene: FlyBase:ras

A:Cross-references: FlyBase:FBgn0003204

C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule

A:Pathway: purine nucleotide biosynthesis

C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo

C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio

F;52-117/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F;138-189/Domain: CBS homology <CBS1>
F;202-249/Domain: CBS homology <CBS2>
F;250-499/Domain: IMP dehydrogenase catalytic homology <IDHC>
F;350/Active site: Cys #status predicted

Query Match 6.0%; Score 23; DB 1; Length 537;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 EAPGEYFFSDGVRLLKKYRGMGSL 287
|||||
Db 414 EAPGEYFFSDGVRLLKKYRGMGSL 436

RESULT 7
S59402
IMP dehydrogenase (EC 1.1.1.205) YLR432w - yeast (Saccharomyces cerevisiae)
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein L9553.4
C:Species: Saccharomyces cerevisiae
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 23-Mar-2001
C:Accession: S59402

R:Du, Z.
submitted to the EMBL Data Library, February 1995
A:Description: The sequence of S. cerevisiae cosmid 9753.

A:Reference number: S53391
A:Accession: S59402
A:Molecule type: DNA
A:Residues: 1-523 <DUZ>
A:Cross-references: EMBL:U01094; NID:g665967; PIDN:AAB67516.1; PID:g665971; GSPDB:GN0001
A:Experimental source: strain S288C (AB972)
C:Genetics:
A:Gene: MIPS:YLR432w
A:Map position: 12R

C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of water
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F;37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F;187-235/Domain: CBS homology <CBS>
F;236-484/Domain: IMP dehydrogenase catalytic homology <IDHC>
F;335/Active site: Cys #status predicted

Query Match 5.5%; Score 21; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVNACGRPGQTAVY 218
|||||
Db 332 GSICITQEVNACGRPGQTAVY 352

RESULT 8
S48997
IMP dehydrogenase (EC 1.1.1.205) PUR5 - yeast (Saccharomyces cerevisiae)
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein YHR216w
C:Species: Saccharomyces cerevisiae
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 23-Mar-2001
C:Accession: S48997

R:Macri, C.
submitted to the EMBL Data Library, February 1994
A:Description: The sequence of S. cerevisiae cosmid 9177.

A:Reference number: S48997
A:Accession: S48997
A:Molecule type: DNA
A:Residues: 1-523 <MAC>
A:Cross-references: EMBL:U00029; NID:g551322; PIDN:AAB69728.1; PID:g458916; GSPDB:GN0000
C:Genetics:
A:Gene: PUR5; MIPS:YHR216w
A:Map position: 8R

C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of water
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F;37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F;187-235/Domain: CBS homology <CBS>
F;236-484/Domain: IMP dehydrogenase catalytic homology <IDHC>
F;335/Active site: Cys #status predicted

Query Match 5.5%; Score 21; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVNACGRPGQTAVY 218
|||||
Db 332 GSICITQEVNACGRPGQTAVY 352

RESULT 9
S50890
IMP dehydrogenase (EC 1.1.1.205) YML056c - yeast (Saccharomyces cerevisiae)
N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein YM9958.06c
C:Species: Saccharomyces cerevisiae
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: S50890

R:Devlin, K.; Churcher, C.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49800

A:Accession: S50890
A:Molecule type: DNA
A:Residues: 1-524 <DEV>
A:Cross-references: EMBL:Z46729; NID:g577134; PIDN:CAA86719.1; PID:g577140; GSPDB:GN0
C:Genetics:
A:Gene: MIPS:YML056c
A:Map position: 13L
A:Introns: 154/1

C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of water
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F;38-104/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F;188-236/Domain: CBS homology <CBS>
F;237-485/Domain: IMP dehydrogenase catalytic homology <IDHC>
F;336/Active site: Cys #status predicted

Query Match 5.5%; Score 21; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVNACGRPGQTAVY 218
|||||
Db 333 GSICITQEVNACGRPGQTAVY 353

RESULT 10
JC7305
IMP dehydrogenase (EC 1.1.1.205) - Bacillus cereus
C:Species: Bacillus cereus
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 24-Oct-2000
C:Accession: JC7305; PC7088
R:Kim, S. I.; Miyamoto, T.; Honjoh, K.; Iio, M.; Hatano, S.

Biosci. Biotechnol. Biochem. 64, 1210-1216, 2000
A:Title: Molecular cloning, overproduction and characterization of the Bacillus cereus
A:Reference number: JC7305
A:Accession: JC7305
A:Molecule type: DNA
A:Residues: 1-509 <KIM>
A:Cross-references: DDBJ:AB035643
A:Experimental source: strain ts-4

A:Accession: PC7088
 A:Molecule type: protein
 A:Residues: 1-7 <KI2>
 C:Genetics:
 A:Gene: impdh
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
 C:Keywords: DNA binding; GMP biosynthesis; NAD; oxidoreductase; sporulation
 F:308/Active site: Cys #status predicted

Query Match 3.6%; Score 14; DB 2; Length 509;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 70 MDTVTEADMAIAMA 83
 |||||
 Db 51 MDTVTEADMAIAMA 64

RESULT 11

A38668
 IMP dehydrogenase (EC 1.1.1.205) - Leishmania donovani
 N:Alternate names: IMPDH; inosine 5'-monophosphate dehydrogenase
 C:Species: Leishmania donovani
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 16-Jul-1999
 C:Accession: A38668
 R:Wilson, K.; Collart, F.R.; Huberman, E.; Stringer, J.R.; Ullman, B.
 J. Biol. Chem. 266: 1665-1671, 1991
 A:Title: Amplification and molecular cloning of the IMP dehydrogenase gene of Leishmania
 A:Reference number: A38668; MUID:91107664
 A:Accession: A38668
 A:Molecule type: DNA
 A:Residues: 1-514 <WIL>
 A:Cross-references: GB:M55667; NID:g159360
 C:Function:
 A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
 A:Pathway: purine nucleotide biosynthesis
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
 C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
 F:28-94/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:179-228/Domain: CBS homology <CBS>
 F:229-472/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:327/Active site: Cys #status predicted

Query Match 3.6%; Score 14; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 208 ACGRPGQTAVYKVA 221
 |||||
 Db 334 ACGRPGQTAVYKVA 347

RESULT 12

S53477
 IMP dehydrogenase (EC 1.1.1.205) FUN63 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH); protein YAR073w
 C:Species: Saccharomyces cerevisiae
 C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
 C:Accession: S53477
 R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Kabac
 submitted to the EMBL Data Library, February 1994
 A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the
 A:Reference number: S53477
 A:Accession: S53477
 A:Molecule type: DNA
 A:Residues: 1-403 <BUS>
 A:Cross-references: EMBL:L28920; NID:g1616966; PIDN:AAC09509.1; PID:g456156; GSPDB:GN000
 C:Genetics:
 A:Gene: FUNG3; MIPS:YAR073w
 A:Map position: 1R
 C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecul
 A:Pathway: purine nucleotide biosynthesis
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
 C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
 F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:187-235/Domain: CBS homology <CBS>
 F:236-403/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:335/Active site: Cys #status predicted

Query Match 3.4%; Score 13; DB 1; Length 403;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 206 VMACGRPOGTAVY 218
 |||||
 Db 340 VMACGRPOGTAVY 352

RESULT 13

T32709
 IMP dehydrogenase (EC 1.1.1.205) T22D1.3 - Caenorhabditis elegans
 N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine 5'-monophosphate dehydroge
 C:Species: Caenorhabditis elegans
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000
 C:Accession: T32709
 R:Geisel, C.; Bradshaw, H.; Hawkins, M.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid T22D1.
 A:Reference number: T21211
 A:Accession: T32709
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-499 <GET>
 A:Cross-references: EMBL:AF039052; PIDN:AAB94282.1; GSPDB:GN000022; CESP:T22D1.3
 A:Experimental source: strain Bristol N2; clone T22D1
 C:Genetics:
 A:Gene: CESP:T22D1.3
 A:Map position: 4
 A:Introns: 35/2; 85/3; 159/1; 183/3; 342/1; 412/3; 493/2
 C:Function:

A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecul
 A:Pathway: purine nucleotide biosynthesis
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
 C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide bio
 F:32-98/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:120-170/Domain: CBS homology <CBS1>
 F:188-238/Domain: CBS homology <CBS2>
 F:239-461/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:337/Active site: Cys #status predicted

Query Match 3.4%; Score 13; DB 1; Length 499;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 259 LLAATTEAPGEYF 271
 |||||
 Db 395 LLAATTEAPGEYF 407

RESULT 14

T40127
 IMP dehydrogenase (EC 1.1.1.205) SPBC2F12.14c - fission yeast (Schizosaccharomyces po
 N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; inosine 5'-monophosphate dehydroge
 C:Species: Schizosaccharomyces pombe
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 21-Jul-2000
 C:Accession: T40127; T42083
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, June 1997
 A:Reference number: T21907
 A:Accession: T40127
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-524 <MOO>
A:Cross-references: EMBL:Z97211; PIDN:CAB10161.1; GSPDB:GN00067; SPDB:SPBC2F12.14c
A:Experimental source: strain 972b-; cosmid c2f12
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722
A:Accession: T42083
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 62-252, 'G', 254-262, 'P', 264-293 <YOS>
A:Cross-references: EMBL:D89106; NID:g1749419; PIDN:BA13769.1; PID:g1749420
A:Experimental source: strain PR745
C:Genetics:
A:Gene: SPDB:SPBC2F12.14c
A:Map position: 2
A:Introns: 153/1
C:Function:
A:Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of
A:Pathway: purine nucleotide biosynthesis
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
F:37-103/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:124-174/Domain: CBS homology <CBS1>
F:187-237/Domain: CBS homology <CBS2>
F:238-486/Domain: IMP dehydrogenase catalytic homology <IDHC>
F:337/Active site: Cys #status predicted

Query Match 3.4%; Score 13; DB 1; Length 524;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 CITQEVNACGRPQ 213
|||||
Db 337 CITQEVNACGRPQ 349

RESULT 15
F86298
IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C:Accession: F86298
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: F86298
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-502 <STO>
A:Cross-references: GB:AE005172; NID:g4966356; PIDN:AAD34687.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1
C:Keywords: GMP biosynthesis; NAD; oxidoreductase

Query Match 2.9%; Score 11; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGVDGLRVGMG 196
|||||
Db 306 AGVDGLRVGMG 316

RESULT 16
JC4999
IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JC4999
R:Collart, F.R.; Osipiuk, J.; Trent, J.; Olsen, G.J.; Huberman, E.
Gene 174, 217-220, 1996
A:Title: Cloning and characterization of the gene encoding IMP dehydrogenase from Ara
A:Reference number: JC4999; MUID:97045815
A:Accession: JC4999
A:Molecule type: DNA
A:Residues: 1-503 <COL>
A:Cross-references: GB:L34684; NID:g1100062; PIDN:AAB41940.1; PID:g11000063
C:Genetics:
A:Gene: impdh
A:Introns: 135/1; 334/3; 404/3; 490/3
C:Complex: homotetramer
C:Function:
A:Description: provides precursors for DNA and RNA biosynthesis; it catalyzes the con
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
F:20-86/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
F:172-220/Domain: CBS homology <CBS2>
F:221-465/Domain: IMP dehydrogenase catalytic homology <IMP>
F:322/Active site: Cys #status predicted

Query Match 2.9%; Score 11; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGVDGLRVGMG 196
|||||
Db 307 AGVDGLRVGMG 317

RESULT 17
D83652
inositol-monophosphate dehydrogenase guaB [imported] - Bacillus halodurans (strain C-
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: D83652
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: D83652
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-485 <STO>
A:Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BA803739.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: guaB
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo

Query Match 2.6%; Score 10; DB 2; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPITADGGI 237
|||||
Db 333 GVPITADGGI 342

RESULT 18
D97232
IMP dehydrogenase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
 C:Accession: D97232
 R:Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum ATCC8254
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: D97232
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-485 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK80647.1; PID:gl5025734; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC8254
 C:Genetics:
 A:Gene: CAC2701
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology

Query Match 2.6%; Score 10; DB 2; Length 485;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPFIADGGI 237
 Db 331 GVPFIADGGI 340
 |||||

RESULT 19
 H95270
 probable kinase/esterase [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid F
 C:Species: Sinorhizobium meliloti
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: H95270
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, L.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C. Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: H95270
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-742 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK64730.1; PID:gl4523133; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSymA
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, F.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hymen, R.W.; Jones, T. Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: Sma0137
 A:Genome: plasmid

Query Match 2.6%; Score 10; DB 2; Length 742;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 AIAAMLMGGI 88
 Db 27 AIAAMLMGGI 36
 |||||

RESULT 20
 D72631
 probable IMP dehydrogenase (EC 1.1.1.205) APE1507 [similarity] - Aeropyrum pernix (strain N)
 N:Alternate names: IMP:NAD+ oxidoreductase; IMPDH; Inosine-5'-monophosphate dehydrogenase
 C:Species: Aeropyrum pernix
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Jun-2000

C:Accession: D72631
 R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tanaka, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
 A:Reference number: A72450; MUID:99310339
 A:Accession: D72631
 A:Molecule type: DNA
 A:Residues: 1-444 <KAW>
 A:Cross-references: DBJ:AP000061; NID:g5104821; PIDN:BAA80506.1; PID:g5105192
 A:Experimental source: strain K1
 C:Comment: This sequence is very similar to IMP dehydrogenase at the amino end and at the latter, the two CBS domains are missing or degenerate.
 C:Genetics:
 A:Gene: APE1507
 C:Superfamily: Lyme disease spirochete IMP dehydrogenase homolog; IMP dehydrogenase
 C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
 F:25-91/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:174-417/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:271/Active site: Cys #status predicted

Query Match 2.3%; Score 9; DB 1; Length 444;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTE 75
 Db 62 SSPMDTVTE 70
 |||||

RESULT 21
 C72264
 IMP dehydrogenase (EC 1.1.1.205) - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: C72264
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M. Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316
 A:Accession: C72264
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-482 <ARN>
 A:Cross-references: GB:AE001789; GB:AE000512; NID:g4981904; PIDN:AAD36418.1; PID:g4981904
 A:Experimental source: strain MSB8
 C:Genetics:
 A:Gene: TM1347
 C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
 C:Keywords: GMP biosynthesis; NAD; oxidoreductase
 F:5-71/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:154-202/Domain: CBS homology <CBS>
 F:203-444/Domain: IMP dehydrogenase catalytic homology <IDC>
 F:301/Active site: Cys #status predicted

Query Match 2.3%; Score 9; DB 2; Length 482;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 VPIIADGGI 237
 Db 329 VPIIADGGI 337
 |||||

RESULT 22
 S54810
 probable oxygenase - Streptomyces fradiae
 C:Species: Streptomyces fradiae
 C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 24-Sep-1999

C;Accession: S54810
 R;Decker, H.; Haag, S.
 Submitted to the EMBL Data Library, May 1995
 A;Description: Cloning and characterization of a polyketide synthase from Streptomyces
 y involved in its oxygenation.
 A;Reference number: S54810
 A;Accession: S54810
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-495 <DEC>
 A;Cross-references: EMBL:X87093; NID:g809102; PIDN:CRA60567.1; PID:g809103
 C;Superfamily: tetracycline 6-hydroxylase

Query Match 2.3%; Score 9; DB 2; Length 495;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 AGVDVIVLD 144
 Db 24 AGVDVIVLD 32

RESULT 23
 G64501
 IMP dehydrogenase (EC 1.1.1.205) - Methanococcus jannaschii
 C;Species: Methanococcus jannaschii
 C;Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 21-Jul-2000
 C;Accession: G64501
 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 reisch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
 A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A;Reference number: A64300; MUID:96337999
 A;Accession: G64501
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-496 <BUL>
 A;Cross-references: GB:U67602; GB:L77117; NID:g1592214; PIDN:AAB99638.1; PID:g1592337;
 C;Genetics:
 A;Map position: FOR1591580-1593070
 A;Start codon: TTG
 C;Function:
 A;Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule
 A;Pathway: purine nucleotide biosynthesis
 C;Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
 C;Keywords: duplication; GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosyn
 F;13-78/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F;99-147/Domain: CBS homology <CBS1>
 F;159-207/Domain: CBS homology <CBS2>
 F;208-458/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F;306/Active site: Cys #status Predicted

Query Match 2.3%; Score 9; DB 1; Length 496;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 229 VPIADGGI 237
 Db 334 VPIADGGI 342

RESULT 24
 A55407
 IMP dehydrogenase (EC 1.1.1.205) - Trypanosoma brucei
 N;Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH)
 C;Species: Trypanosoma brucei
 C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 16-Jul-1999
 C;Accession: A55407
 R;Wilson, K.; Berens, R.L.; Sifri, C.D.; Ullman, B.

J. Biol. Chem. 269, 28979-28987, 1994
 A;Title: Amplification of the inosinate dehydrogenase gene in Trypanosoma brucei gamb
 A;Reference number: A55407; MUID:95050714
 A;Accession: A55407
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-512 <WIL>
 A;Cross-references: GB:M97794; NID:gl62135; PIDN:AAB46420.1; PID:g162136
 A;Note: authors translated the codon CGT for residue 76 as Leu
 C;Genetics:
 A;Gene: impdh
 C;Function:
 A;Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule
 A;Pathway: purine nucleotide biosynthesis
 C;Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homo
 C;Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis
 F;26-92/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F;177-226/Domain: CBS homology <CBS>
 F;227-470/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F;325/Active site: Cys #status Predicted

Query Match 2.3%; Score 9; DB 1; Length 512;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SSPMDVTVE 75
 Db 63 SSPMDVTVE 71

RESULT 25
 GNFG1
 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) retr
 N;Contains: retropepsin (EC 3.4.23.16)
 C;Species: Drosophila melanogaster
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 16-Jul-1999
 C;Accession: B25666; A23769
 R;Marlor, R.L.; Parkhurst, S.M.; Corces, V.G.
 Mol. Cell. Biol. 6, 1129-1134, 1986
 A;Title: The Drosophila melanogaster gypsy transposable element encodes putative gene
 A;Reference number: A93071; MUID:87064379
 A;Accession: B25666
 A;Molecule type: DNA
 A;Residues: 1-1035 <MAR>
 A;Note: the authors translated the codons CAG for residue 99 and CAA for residue 710
 R;Yuki, S.; Ishimaru, S.; Inouye, S.; Saigo, K.
 Nucleic Acids Res. 14, 3017-3030, 1986
 A;Title: Identification of genes for reverse transcriptase-like enzymes in two Drosop
 s.

A;Reference number: A23769; MUID:86176782
 A;Accession: A23769
 A;Molecule type: DNA
 A;Residues: 21-30,'AR',33-59,'R',61-231,'S',233-489,'V',491-882,'T',884-922,'S',924-9
 A;Cross-references: GB:X03734; NID:g8036; PIDN:CAA27371.1; PID:g929567
 C;Genetics:
 A;Gene: FlyBase:gypsy/pol
 A;Cross-references: FlyBase:FBgn0014966
 C;Superfamily: pol polyprotein
 C;Keywords: aspartic proteinase; hydrolase; polyprotein; reverse transcriptase
 F;5-106/Product: retropepsin #status predicted <RPP>
 F;29/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 2.3%; Score 9; DB 1; Length 1035;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 130 LDLLTQAGV 138
 Db 94 LDLLTQAGV 102

RESULT 26
H72054
ribosomal protein S17 CP0109 [imported] - Chlamydophila pneumoniae (strains CWL029 and A
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C:Accession: H72054; A81612
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606
C:Accession: H72054
A:Molecule type: DNA
A:Residues: 1-86 <ARN>
A:CROSS-references: GB:AE001647; GB:AE001363; NID:g4376920; PIDN:AAD18777.1; PID:g437693
A:Experimental source: strain CWL029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255
C:Accession: A81612
A:Molecule type: DNA
A:Residues: 1-86 <REA>
A:CROSS-references: GB:AE002173; GB:AE002161; NID:g7189033; PIDN:AAF37992.1; PID:g718904
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: rs17; CP0109
C:Superfamily: Escherichia coli ribosomal protein S17

Query Match 2.1%; Score 8; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 SEGDKVKI 309
|||||
Db 57 SEGDKVKI 64

RESULT 27
C86570
S17 ribosomal protein [imported] - Chlamydophila pneumoniae (strain J138)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C:Accession: C86570
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349
C:Accession: C86570
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <STO>
A:CROSS-references: GB:BA000008; NID:g8979010; PIDN:BAA98845.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: rs17

C:Accession: S78078; S70312
R:Zhong, W.; Louis, E.J.; Bussey, H.
submitted to the EMBL Data Library, August 1996
A:Description: Saccharomyces cerevisiae chromosome I right arm.
A:Reference number: S78078
C:Accession: S78078
A:Molecule type: DNA
A:Residues: 1-157 <ZHO>
A:CROSS-references: EMBL:L28920; NID:g2911244; PID:g2911246; GSPDB:GN00001; MIPS:YARO
A:Note: this is a revision to the sequence from reference S53458
R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Ka
submitted to the EMBL Data Library, February 1994
A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of th
A:Reference number: S53458
C:Accession: S70312
A:Molecule type: DNA
A:Residues: 1-134 <BUS>
A:CROSS-references: EMBL:L28920; GSPDB:GN00001; MIPS:YAR075w
A:Note: This sequence has been revised in reference S78078
C:Comment: This sequence is highly similar to the carboxyl 30% of IMP dehydrogenase
C:Genetics:
A:Gene: MIPS:YAR075w
A:Map position: 1R
C:Superfamily: hypothetical IMP dehydrogenase-related protein YAR075w; IMP dehydrogen
F:1-157/Domain: IMP dehydrogenase catalytic homology #status atypical <IDHC>

Query Match 2.1%; Score 8; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 376 LHSYEKRL 383
|||||
Db 148 LHSYEKRL 155

RESULT 29
AE0160
probable glutathione S-transferase-family protein YP01314 [imported] - Yersinia pesti
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AE0160
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
C:Accession: AE0160
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <KUR>
A:CROSS-references: GB:AL590842; PIDN:CAC90144.1; PID:g15979364; GSPDB:GN00175
C:Genetics:
A:Gene: YP01314
C:Superfamily: hypothetical protein b0838

Query Match 2.1%; Score 8; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 DKVKIAQG 312
|||||
Db 124 DKVKIAQG 131

RESULT 30
C96948
deoxyphosphoglucanate aldolase (gene kdga) [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: C96948

Query Match 2.1%; Score 8; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 SEGDKVKI 309
|||||
Db 57 SEGDKVKI 64

RESULT 28
S78078
IMP dehydrogenase-related protein YAR075w - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999

C:Accession: S78078; S70312
R:Zhong, W.; Louis, E.J.; Bussey, H.
submitted to the EMBL Data Library, August 1996
A:Description: Saccharomyces cerevisiae chromosome I right arm.
A:Reference number: S78078
C:Accession: S78078
A:Molecule type: DNA
A:Residues: 1-157 <ZHO>
A:CROSS-references: EMBL:L28920; NID:g2911244; PID:g2911246; GSPDB:GN00001; MIPS:YARO
A:Note: this is a revision to the sequence from reference S53458
R:Bussey, H.; Keng, T.; Storms, R.K.; Vo, D.; Zhong, W.; Fortin, N.; Barton, A.B.; Ka
submitted to the EMBL Data Library, February 1994
A:Description: Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of th
A:Reference number: S53458
C:Accession: S70312
A:Molecule type: DNA
A:Residues: 1-134 <BUS>
A:CROSS-references: EMBL:L28920; GSPDB:GN00001; MIPS:YAR075w
A:Note: This sequence has been revised in reference S78078
C:Comment: This sequence is highly similar to the carboxyl 30% of IMP dehydrogenase
C:Genetics:
A:Gene: MIPS:YAR075w
A:Map position: 1R
C:Superfamily: hypothetical IMP dehydrogenase-related protein YAR075w; IMP dehydrogen
F:1-157/Domain: IMP dehydrogenase catalytic homology #status atypical <IDHC>

Query Match 2.1%; Score 8; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 376 LHSYEKRL 383
|||||
Db 148 LHSYEKRL 155

RESULT 29
AE0160
probable glutathione S-transferase-family protein YP01314 [imported] - Yersinia pesti
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AE0160
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
C:Accession: AE0160
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <KUR>
A:CROSS-references: GB:AL590842; PIDN:CAC90144.1; PID:g15979364; GSPDB:GN00175
C:Genetics:
A:Gene: YP01314
C:Superfamily: hypothetical protein b0838

Query Match 2.1%; Score 8; DB 2; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 305 DKVKIAQG 312
|||||
Db 124 DKVKIAQG 131

RESULT 30
C96948
deoxyphosphoglucanate aldolase (gene kdga) [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: C96948

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daily, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A;Reference number: A96900; MUID:21359325; PMID:21359325
 A;Accession: C96948
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-208 <KUR>
 A;Cross-references: GB:AE001437; PIDN:AAK78374.1; PID:g15023245; GSPDB:GN00168
 A;Experimental source: Clostridium acetobutylicum ATCC824
 C;Genetics:
 A;Gene: CAC0394
 C;Superfamily: 2-dehydro-3-deoxyphosphogluconate aldolase

Query Match 2.1%; Score 8; DB 2; Length 208;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 VVTAQAQK 181
 |||||
 Db 71 VVTAQAQK 78

RESULT 31
 S73185
 hypothetical protein 254 - red alga (Porphyra purpurea) chloroplast
 C;Species: chloroplast Porphyra purpurea
 C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 24-Sep-1999
 C;Accession: S73185
 R;Reith, M.; Munnholland, J.
 Plant Mol. Biol. Rep. 13, 333-335, 1995
 A;Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.
 A;Reference number: S73108
 A;Accession: S73185
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-254 <REI>
 A;Cross-references: EMBL:U38804; NID:g1276652; PIDN:AAC08150.1; PID:g1276730
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
 C;Genetics:
 A;Genome: chloroplast
 C;Superfamily: conserved hypothetical protein HI0188
 C;Keywords: chloroplast

Query Match 2.1%; Score 8; DB 2; Length 254;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 APGEYFFS 273
 |||||
 Db 78 APGEYFFS 85

RESULT 32
 T09388
 (S)-2-hydroxy-acid oxidase (EC 1.1.3.15) - alfalfa (fragment)
 N;Alternate names: glycolate oxidase
 C;Species: Medicago sativa (alfalfa)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Mar-2001
 C;Accession: T09388
 R;Stout, J.M.; McKersie, B.D.
 submitted to the EMBL Data Library, August 1998
 A;Description: Gene expression in alfalfa.
 A;Reference number: Z14222
 A;Accession: T09388
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-283 <STO>
 A;Cross-references: EMBL:AF082874; NID:g3435305; PID:g3435306
 A;Experimental source: shoot apical meristem

C;Function:
 A;Description: catalyzes oxidation of glycolate to glyoxylate and hydrogen peroxide
 A;Pathway: photorespiratory pathway
 C;Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology
 C;Keywords: flavoprotein; FMN; oxidoreductase; photorespiration
 F;1-212/Domain: (S)-2-hydroxy-acid oxidase homology (fragment) <2HY>
 F;166/Active site: His #status Predicted

Query Match 2.1%; Score 8; DB 2; Length 283;
 Best Local Similarity 100.0%; Pred. No. 8.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
 |||||
 Db 208 KALALGAS 215

RESULT 33
 T07032
 (S)-2-hydroxy-acid oxidase (EC 1.1.3.15) - tomato (fragment)
 N;Alternate names: glycolate oxidase
 C;Species: Lycopersicon esculentum (tomato)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 18-Aug-2000
 C;Accession: T07032
 R;Speirs, J.
 submitted to the EMBL Data Library, November 1995
 A;Reference number: Z15875
 A;Accession: T07032
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-290 <SPE>
 A;Cross-references: EMBL:X92888; NID:g1063399; PIDN:CAA63482.1; PID:g1063400
 A;Experimental source: cultivar breeding line 'de Ruiter 83638'; Young leaf
 C;Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology
 C;Keywords: flavoprotein; FMN; oxidoreductase; photorespiration
 F;1-220/Domain: (S)-2-hydroxy-acid oxidase homology (fragment) <2HY>
 F;174/Active site: His #status Predicted

Query Match 2.1%; Score 8; DB 2; Length 290;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
 |||||
 Db 216 KALALGAS 223

RESULT 34
 H96792
 unknown protein F14G6.10 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C;Accession: H96792
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maftl, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719
 A;Accession: H96792
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-302 <STO>
 A;Cross-references: GB:AE005173; NID:g6642668; PIDN:AAF20248.1; GSPDB:GN00141
 C;Genetics:
 A;Gene: F14G6.10

A:Map position:11
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*
 C:Superfamily: Arabidopsis thaliana hypothetical protein T12H17.200

Query Match 2.1%; Score 8; DB 2; Length 302;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 QVIGGNV 175
 |||||
 Db 197 QVIGGNV 204

RESULT 35
 A71887
 probable GMP reductase (EC 1.6.6.8) - *Helicobacter pylori* (strain J99)
 N:Alternate names: guanosine monophosphate reductase
 C:Species: *Helicobacter pylori*
 A:Variety: strain J99
 C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 16-Jul-1999
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jlang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A:Reference number: A71800; MUID:99120557
 A:Accession: A71887
 A:Molecule type: DNA
 A:Residues: 1-325 <ARN>
 A:Cross-references: GB:AE001509; GB:AE001439; NID:94155350; PIDN:AAD06382.1; PID:9415537
 C:Experimental source: strain J99
 C:Genetics:
 A:Gene: guac
 C:Function:
 A:Description: catalyzes the reductive deamination of GMP into IMP using NADPH
 A:Pathway: purine catabolism
 C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrogena
 C:Keywords: NADP; oxidoreductase; purine catabolism
 F:4-70/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:74-304/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:174/Active site: Cys #status predicted

Query Match 2.1%; Score 8; DB 1; Length 325;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 PIIADGGI 237
 |||||
 Db 202 PIIADGGI 209

RESULT 36
 C70015
 probable GMP reductase (EC 1.6.6.8) yumd - *Bacillus subtilis*
 N:Alternate names: guanosine monophosphate reductase
 C:Species: *Bacillus subtilis*
 C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 16-Jun-2000
 C:Accession: C70015
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 A.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
 ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Roche, E.; Roche, M.; Sadaie, Y.; Sato, T.; Scanlon
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*
 A:Reference number: A69580; MUID:98044033
 A:Accession: C70015
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-326 <KUN>
 A:Cross-references: GB:299120; GB:AL009126; NID:g2635613; PIDN:CAB15203.1; PID:g26357
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yumd
 C:Function:
 A:Description: catalyzes the reductive deamination of GMP into IMP using NADPH
 A:Pathway: purine catabolism
 C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrog
 C:Keywords: NADP; oxidoreductase; purine catabolism
 F:5-71/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:75-305/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:175/Active site: Cys #status predicted

Query Match 2.1%; Score 8; DB 1; Length 326;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 PIIADGGI 237
 |||||
 Db 203 PIIADGGI 210

RESULT 37
 F64626
 probable GMP reductase (EC 1.6.6.8) - *Helicobacter pylori* (strain 26695)
 N:Alternate names: guanosine monophosphate reductase
 C:Species: *Helicobacter pylori*
 C:Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 16-Jul-1999
 C:Accession: F64626
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
 Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
 A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
 A:Reference number: A64520; MUID:97394467
 A:Accession: F64626
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-327 <TOM>
 A:Cross-references: GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07901.1; PID:g231
 C:Function:
 A:Description: catalyzes the reductive deamination of GMP into IMP using NADPH
 A:Pathway: purine catabolism
 C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrog
 C:Keywords: NADP; oxidoreductase; purine catabolism
 F:6-72/Domain: IMP dehydrogenase amino-terminal homology <IDHN>
 F:76-306/Domain: IMP dehydrogenase catalytic homology <IDHC>
 F:176/Active site: Cys #status predicted

Query Match 2.1%; Score 8; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 PIIADGGI 237
 |||||
 Db 204 PIIADGGI 211

RESULT 38
 D97326
 GMP reductase [imported] - *Clostridium acetobutylicum*
 C:Species: *Clostridium acetobutylicum*
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
 C:Accession: D97326

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum ATCC824
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: D97326
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK81399.1; PID:g15026562; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrogenase

Query Match 2.1%; Score 8; DB 2; Length 327;

Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237

Db 203 PIIADGGI 210

RESULT 39

A95145

conserved hypothetical protein SP1249 [imported] - Streptococcus pneumoniae (strain TIGR
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001

R:Accession: A95145

R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Helgerson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: A95145

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-328 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK75354.1; PID:g14972731; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP1249

C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrogenase

Query Match 2.1%; Score 8; DB 2; Length 328;

Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237

Db 204 PIIADGGI 211

RESULT 40

G98012

GMP reductase [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae

C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001

R:Accession: G98012

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Eisele, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: G98012

A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-328 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99931.1; PID:g15458756; GSPDB:GN00174
C:Genetics:
A:Gene: guaC
C:Superfamily: GMP reductase; IMP dehydrogenase amino-terminal homology; IMP dehydrogenase

Query Match 2.1%; Score 8; DB 2; Length 328;

Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237

Db 204 PIIADGGI 211

Search completed: September 26, 2002, 08:34:44

Job time: 318 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:32:22 ; Search time 13.39 Seconds
(without alignments)
1110.404 Million cell updates/sec

Title: US-09-853-918-30
Perfect score: 384
Sequence: 1 MADYLISGCTGYVPEDSLTA.....MSAQIEGGVHGLSHYEKRLY 384

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	271	70.6	514	1	IMD1_HUMAN
2	87	22.7	514	1	IMD1_MOUSE
3	31	8.1	514	1	IMD2_HUMAN
4	31	8.1	514	1	IMD2_MESAU
5	31	8.1	514	1	IMD2_MOUSE
6	23	6.0	537	1	IMDH_DROME
7	21	5.5	521	1	IMH3_CANAL
8	21	5.5	523	1	IMH1_YEAST
9	21	5.5	523	1	IMH2_YEAST
10	21	5.5	524	1	IMH3_YEAST
11	14	3.6	514	1	IMDH_LEIDO
12	13	3.4	403	1	IMH4_YEAST
13	11	2.9	502	1	IMH2_ARATH
14	11	2.9	503	1	IMH1_ARATH
15	9	2.3	454	1	IMDH_PNECA
16	9	2.3	496	1	IMDH_METJA
17	9	2.3	512	1	IMDH_TRYBB
18	9	2.3	1035	1	POLY_DROME
19	8	2.1	86	1	RS17_CHLPN
20	8	2.1	254	1	YC43_PORPU
21	8	2.1	367	1	GOX1_ARATH
22	8	2.1	367	1	GOX2_ARATH
23	8	2.1	368	1	Y165_RICPR
24	8	2.1	393	1	MDLB_PSEPU
25	8	2.1	481	1	IMDH_HELPJ
26	8	2.1	481	1	IMDH_HELPY
27	8	2.1	490	1	IMDH_AQUAE
28	8	2.1	498	1	IMDH_RHTR
29	8	2.1	521	1	IMDH_CHLVI
30	7	1.8	163	1	Y22B_HAEIN
31	7	1.8	180	1	IF3_XYLFA
32	7	1.8	181	1	IF3_RHOSH
33	7	1.8	187	1	PPIA_PSEAE

RESULT 1

ALIGNMENTS

34	7	1.8	193	1	YBF9_YEAST
35	7	1.8	227	1	MTR2_MOUSE
36	7	1.8	282	1	Y134_METJA
37	7	1.8	282	1	YEA5_YEAST
38	7	1.8	290	1	YCA3_GUTH
39	7	1.8	297	1	CD20_HUMAN
40	7	1.8	306	1	PYRD_METJA
41	7	1.8	319	1	MER4_STRLI
42	7	1.8	333	1	YCA8_CYAPA
43	7	1.8	334	1	DMC1_YEAST
44	7	1.8	334	1	HMU1_YERPE
45	7	1.8	351	1	HAO2_HUMAN
46	7	1.8	352	1	HAO3_RAT
47	7	1.8	353	1	HAO3_HUMAN
48	7	1.8	369	1	GOX_SPIOL
49	7	1.8	370	1	HAO1_HUMAN
50	7	1.8	370	1	HAO1_MOUSE
51	7	1.8	384	1	FHUB_BACSU
52	7	1.8	404	1	IMDH_BORBU
53	7	1.8	405	1	AATC_RHIME
54	7	1.8	412	1	YG08_SYNY3
55	7	1.8	435	1	COBB_PSEAE
56	7	1.8	442	1	GLXD_RHIME
57	7	1.8	444	1	VGLX_HSVBS
58	7	1.8	457	1	CD4_MOUSE
59	7	1.8	466	1	BIAR_MOUSE
60	7	1.8	466	1	BIAR_RAT
61	7	1.8	467	1	BIAR_SHEEP
62	7	1.8	468	1	BIAR_PIG
63	7	1.8	473	1	BIAR_CANFA
64	7	1.8	474	1	BIAR_FELCA
65	7	1.8	485	1	IMDH_PYRAB
66	7	1.8	485	1	IMDH_PYRFU
67	7	1.8	486	1	IMDH_PYRHO
68	7	1.8	487	1	IMDH_PASMU
69	7	1.8	488	1	IMDH_ACICA
70	7	1.8	488	1	IMDH_ECOLI
71	7	1.8	488	1	IMDH_HAEIN
72	7	1.8	491	1	GABD_RHISN
73	7	1.8	492	1	IMDH_STRPY
74	7	1.8	513	1	IMDH_BACSU
75	7	1.8	528	1	YC79_MYCTU
76	7	1.8	529	1	IMDH_MYCLE
77	7	1.8	529	1	IMDH_MYCTU
78	7	1.8	549	1	BETA_RHIME
79	7	1.8	559	1	RS1_BUCAP
80	7	1.8	561	1	EST1_MESAU
81	7	1.8	563	1	METB_ARATH
82	7	1.8	571	1	UVRC_MYCBV
83	7	1.8	614	1	BTUB_SALTY
84	7	1.8	614	1	SPKE_SYNY3
85	7	1.8	700	1	PALY_WHEAT
86	7	1.8	700	1	YNCB_ECOLI
87	7	1.8	770	1	ACE2_YEAST
88	7	1.8	811	1	MUTS_THAEQ
89	7	1.8	824	1	NSFH_CAEEL
90	7	1.8	902	1	SYG1_YEAST
91	7	1.8	917	1	GLRK_LYMST
92	7	1.8	946	1	K6P2_CANAL
93	7	1.8	1025	1	MK21_YEAST
94	7	1.8	1032	1	Y895_HAEIN
95	7	1.8	1128	1	NGP1_HUMAN
96	7	1.8	1128	1	NGP1_RAT
97	7	1.8	1453	1	CAL1_CHICK
98	7	1.8	1569	1	YFJA_ECOLI
99	7	1.8	2284	1	POLI_GFLV
100	7	1.8	2747	1	FAP_DROME

P34224	saccharomyc
Q922d1	mus musculus
Q57598	methanococc
P40003	saccharomyc
O78493	quillardia
P11836	homo sapien
Q58070	methanococc
P30344	streptomyces
P48325	cyanophora
P25453	saccharomyc
Q56992	versinia pe
Q9dyq3	homo sapien
Q07523	rattus norv
Q9dyq2	homo sapien
P05414	spinacia ol
Q9ujm8	homo sapien
Q9wu19	mus musculus
P49936	bacillus su
P49058	borrelia bu
O87320	rhizobium m
P73001	synechocyst
O91471	pseudomonas
O87392	rhizobium m
Q08103	bovine herp
P06332	mus musculus
P34971	mus musculus
P18090	rattus norv
Q28927	ovis aries
Q28998	sus scrofa
P79148	canis faml
Q9est6	felis silve
Q9uy49	pyrococcus
P42851	pyrococcus
O58045	pyrococcus
Q916b7	pasteurella
P31002	acinetobact
P06981	escherichia
P44334	haemophilus
P55653	rhizobium s
P50099	streptococc
P21879	bacillus su
Q11038	mycobacteri
Q49729	mycobacteri
Q50715	mycobacteri
P54223	rhizobium m
Q44653	buchnera ap
Q64419	mesocricetu
P55217	arabidopsis
O84898	mycoplasma
P37409	salmonella
P73515	synechocyst
Q43210	tritium ae
P76115	escherichia
P21192	saccharomyc
Q56215	thermus aqu
Q94392	caenorhabdi
P40528	saccharomyc
P26591	lymnaea sta
O94200	candida alb
Q12176	saccharomyc
Q57124	haemophilus
Q9y2a7	homo sapien
P55161	rattus norv
P02457	gallus gall
P52143	escherichia
P29149	grapevine f
P55824	drosophila

KW Multigene family; Repeat: CBS domain.
 FT DOMAIN 112 167 CBS 1.
 FT BINDING 177 232 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL).
 SQ SEQUENCE 514 AA; 55294 MW; B38AA2EB0ECC4CE CRC64;

Query Match 22.7%; Score 87; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 7.2e-78;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 DSSQNSVYQIAMVHIKQYKYPHLQVIGNVVTAQAQKNLIDAGVGLRVGMCSSICIT 203
 |||||
 Db 274 DSSQNSVYQIAMVHIKQYKYPHLQVIGNVVTAQAQKNLIDAGVGLRVGMCSSICIT 333
 |||||

QY 204 QEVMAQGRPGQTAVYKVAEYARFGVP 230
 |||||
 Db 334 QEVMAQGRPGQTAVYKVAEYARFGVP 360
 |||||

RESULT 3
 IMD2_HUMAN
 ID IMD2_HUMAN STANDARD; PRT; 514 AA.
 AC P12268;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
 dehydrogenase 2) (IMPDH-II) (IMPD 2).
 GN IMPDH2 OR IMPD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=89008491; PubMed=2902093;
 RA Collart F.R., Huberman E.;
 RT "Cloning and sequence analysis of the human and Chinese hamster
 RT inosine-5'-monophosphate dehydrogenase cDNAs.";
 RL J. Biol. Chem. 263:15769-15772(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=90203022; PubMed=1969416;
 RA Natsumeda Y., Ohno S., Kawasaki H., Konno Y., Weber G., Suzuki K.;
 RT "Two distinct cDNAs for human IMP dehydrogenase.";
 RL J. Biol. Chem. 265:5292-5295(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95091778; PubMed=7999076;
 RA Glesne D.A., Huberman E.;
 RT "Cloning and sequence of the human type II IMP dehydrogenase gene.";
 RL Biochem. Biophys. Res. Commun. 205:537-544(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95204479; PubMed=7896827;
 RA Zimmermann A.G., Spychala J., Mitchell B.S.;
 RT "Characterization of the human inosine-5'-monophosphate dehydrogenase
 RT type II gene.";
 RL J. Biol. Chem. 270:6808-6814(1995).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=95283610; PubMed=7763314;
 RA Hager P.W., Collart F.R., Huberman E., Mitchell B.S.;
 RT "Recombinant human inosine monophosphate dehydrogenase type I and
 RT type II proteins. Purification and characterization of inhibitor
 RT binding.";
 RL Biochem. Pharmacol. 49:1323-1329(1995).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=99199217; PubMed=10097070;

RA Colby T.D., Vanderveen K., Strickler M.D., Markham G.D.,
 RA Goldstein B.M.;
 RT "Crystal structure of human type II inosine monophosphate
 RT dehydrogenase: Implications for ligand binding and drug design.";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:3531-3536(1999).
 CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- TISSUE SPECIFICITY: IMP TYPE I IS THE MAIN SPECIES IN NORMAL
 CC LEUKOCYTES AND TYPE II PREDOMINATES OVER TYPE I IN THE TUMOR.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC -----
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 CC -----
 CC EMBL; J04208; AAA36112.1; -;
 CC EMBL; L33842; AAA67054.1; -;
 CC EMBL; L39210; AAB70699.1; -;
 CC PIR; A31997; A31997.
 CC PIR; B35566; B35566.
 CC PDB; 1B30; 12-APR-99.
 CC MIM; 146691; -;
 CC InterPro; IPR000644; CBS.
 CC InterPro; IPR003009; FMN_enzyme.
 CC InterPro; IPR001093; IMP_DH_GMP_RED.
 CC Pfam; PF00571; CBS; 2.
 CC Pfam; PF00478; IMPDH_C; 1.
 CC Pfam; PF01574; IMPDH_N; 1.
 CC SMART; SM00116; CBS; 2.
 CC PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 CC Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
 KW Multigene family; Repeat: CBS domain; 3D-structure.
 FT DOMAIN 112 167 CBS 1.
 FT BINDING 177 232 CBS 2.
 FT BINDING 331 331 IMP (POTENTIAL).
 FT CONFLICT 190 191 AG -> RS (IN REF. 1).
 SQ SEQUENCE 514 AA; 55805 MW; 876BEA0EC1DDBEE9 CRC64;

Query Match 8.1%; Score 31; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 1.4e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGMSLLAATTEAPGEYFFSDG 275
 |||||
 Db 375 KALALGASTVMGMSLLAATTEAPGEYFFSDG 405
 |||||

RESULT 4
 IMD2_MESAU
 ID IMD2_MESAU STANDARD; PRT; 514 AA.
 AC P12269;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
 dehydrogenase 2) (IMPDH-II) (IMPD 2).
 GN IMPDH2 OR IMPDH.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 336-370.
 RX MEDLINE=89008491; PubMed=2902093;
 RA Collart F.R., Huberman E.;
 RT "Cloning and sequence analysis of the human and Chinese hamster
 RT Inosine-5'-monophosphate dehydrogenase cDNAs.";
 RL J. Biol. Chem. 263:15769-15772(1988).
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC CATALYTIC ACTIVITY: Inosine 5'-phosphate + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 CC -----
 DR EMBL; J04209; AAA36993.1; -;
 DR PIR; B31997; B31997.
 DR HSSP; P12268; 1B30.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
 KW Multigene family; Repeat; CBS domain.
 FT DOMAIN 112 167
 FT BINDING 177 232 CBS 1.
 FT VARIANT 331 333 IMP (POTENTIAL).
 FT BINDING 331 331 IMP (POTENTIAL).
 FT VARIANT 333 333
 FT VARIANT 351 351
 FT CONFLICT 483 483
 FT SEQUENCE 514 AA; 55890 MW; 5FA0138FA41E8A02 CRC64;
 Query Match 8.1%; Score 31; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 1.4e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 KALALGASTVMMGSLAATTEAPGEYFFSDG 275
 Db 375 KALALGASTVMMGSLAATTEAPGEYFFSDG 405
 RESULT 5
 IMD2_MOUSE
 ID IMD2_MOUSE STANDARD; PRT; 514 AA.
 AC P24547; Q61734;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase 2 (EC 1.1.1.205) (IMP
 DE dehydrogenase 2) (IMPDH-II) (IMPD 2).
 GN IMPDH2 OR IMPDH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10050;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=91153661; PubMed=1671845;
 RA Tiedeman A.A., Smith J.M.;
 RT "Isolation and sequence of a cDNA encoding mouse IMP dehydrogenase.";
 RL Gene 97:289-293(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS MYCOPHENOLIC ACID RESISTANT.
 RC TISSUE=Brain;
 RX MEDLINE=94153991; PubMed=7906545;
 RA Lightfoot T., Snyder F.F.;
 RT "Gene amplification and dual point mutations of mouse IMP
 RT dehydrogenase associated with cellular resistance to mycophenolic
 RT acid.";
 RL Biochim. Biophys. Acta 1217:156-162(1994).
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH. IT MAY ALSO HAVE A ROLE IN THE DEVELOPMENT OF
 CC MALIGNANCY AND THE GROWTH PROGRESSION OF SOME TUMORS.
 CC CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 CC -----
 DR EMBL; M33934; AAA39311.1; -;
 DR EMBL; M98333; AAA20181.1; -;
 DR PIR; JT0565; JT0565.
 DR HSSP; P12268; 1B30.
 DR MGD; MGI:109367; Impdh2.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
 KW Multigene family; Repeat; CBS domain.
 FT DOMAIN 112 167
 FT BINDING 177 232 CBS 1.
 FT BINDING 331 331 IMP (POTENTIAL).
 FT VARIANT 333 333
 FT VARIANT 351 351
 FT CONFLICT 483 483
 FT SEQUENCE 514 AA; 55785 MW; D5B66A5C5EBC421 CRC64;
 Query Match 8.1%; Score 31; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 1.4e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 KALALGASTVMMGSLAATTEAPGEYFFSDG 275
 Db 375 KALALGASTVMMGSLAATTEAPGEYFFSDG 405
 RESULT 6
 IMDH_DROME
 ID IMDH_DROME STANDARD; PRT; 537 AA.
 AC Q07152; Q26455; Q9W2R8;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
 DE dehydrogenase) (IMPDH) (IMPD) (Raspberry protein).
 GN RAS OR CG1799.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Nash D., Hu S.;
 RT "Drosophila inosine monophosphate dehydrogenase is encoded at the
 RT raspberry locus";
 RL (In) Abstracts of the 35th meeting of the Canadian Federation of
 RL Biological Societies, pp.72-72, Victoria (1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=94259281; PubMed=7911114;
 RA Nash D., Hu S., Leonard N.J., Tjong S.Y., Phillips D.;
 RT "The raspberry locus of Drosophila melanogaster includes an inosine
 RT monophosphate dehydrogenase like coding sequence.";
 RL Genome 37:333-344(1994).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=CANTON-S;
 RX MEDLINE=94114565; PubMed=7904480;
 RA Sifri C.D., Wilson K., Smolik S., Forte M., Ullman B.;
 RT "Cloning and sequence analysis of a Drosophila melanogaster cDNA
 RT encoding IMP dehydrogenase.";
 RL Biochim. Biophys. Acta 1217:103-106(1994).
 RN [4]
 RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RP MEDLINE=96069715; PubMed=7476879;
 RA Sile R., Bowles M.;
 RT "The raspberry locus encodes Drosophila inosine monophosphate
 RT dehydrogenase.";
 RL Mol. Gen. Genet. 248:755-766(1995).
 RN [5]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Randell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aquavani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
 CC OF CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L14847; AAA21831.1; -;
 DR EMBL; L22608; AAA16839.1; -;
 DR EMBL; S80430; AAB35628.1; -;
 DR EMBL; AE003451; AAF46622.1; -;
 DR HSSP; P12268; 1B30.
 DR FlyBase; FBgn0003204; ras.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN_enzyme.
 DR InterPro; IPR010093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
 KW CBS domain.
 FT DOMAIN 134 189 CBS 1.
 FT DOMAIN 198 251 CBS 2.
 FT BINDING 350 350 IMP (BY SIMILARITY).
 FT CONFLICT 38 38 D -> V (IN REF. 4).
 FT CONFLICT 53 53 T -> P (IN REF. 4).
 FT CONFLICT 99 102 EMAL -> RCH (IN REF. 4).
 FT CONFLICT 184 184 D -> A (IN REF. 4).
 FT CONFLICT 194 194 V -> S (IN REF. 4).
 FT CONFLICT 216 217 AN -> EH (IN REF. 4).
 FT CONFLICT 226 229 GKLP -> ATA (IN REF. 4).
 FT CONFLICT 244 244 T -> A (IN REF. 4).
 FT CONFLICT 261 262 KQ -> TR (IN REF. 4).
 FT CONFLICT 265 266 VG -> CP (IN REF. 4).
 FT CONFLICT 277 278 AR -> GCRA (IN REF. 4).
 FT CONFLICT 284 284 A -> R (IN REF. 4).
 FT CONFLICT 301 301 Y -> I (IN REF. 4).
 FT CONFLICT 387 388 QS -> HA (IN REF. 4).
 SQ SEQUENCE 537 AA; 57829 MW; A5EAB41AEAA64EBD CRC64;
 Query Match 6.0%; Score 23; DB 1; Length 537;
 Best Local Similarity 100.0%; Pred. No. 1.2e-14;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 265 EAPGEYFFSDGVRLLKRYGMGSL 287
 Db 414 EAPGEYFFSDGVRLLKRYGMGSL 436
 RESULT 7

```
IMH3_CANAL
ID IMH3_CANAL STANDARD; PRT; 521 AA.
AC O00086;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN IMH3.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=3476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SS;
RX MEDLINE=97234646; PubMed=9079920;
RA Koehler G.A., White T.C., Agabian N.;
RT "overexpression of a cloned IMP dehydrogenase gene of Candida
RT albicans confers resistance to the specific inhibitor mycophenolic
RT acid.";
RL J. Bacteriol. 179:2331-2338(1997).
CC -1- FUNCTION: ESSENTIAL ENZYME IN THE DE NOVO BIOSYNTHESIS OF GMP,
CC CATALYSING THE NAD-DEPENDENT OXIDATION OF IMP TO XMP.
CC -1- CATALYTIC ACTIVITY: inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT EQUAL LEVELS IN THE YEAST OR
CC HYPHAL FORM.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U85049; AAB51509.1; -.
DR HSSP; P12268; LB30.
DR COMPLEYEST-2DPAGE; O00086; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain. 117 172 CBS 1.
FT DOMAIN 180 232 CBS 2.
FT BINDING 333 333 IMP (POTENTIAL).
FT SEQUENCE 521 AA; 56239 MW; 5F1E52611B1E1418 CRC64;
SQ
Query Match 5.5%; Score 21; DB 1; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 GSICITQEVNACGRPGGTAVY 218
Db 330 GSICITQEVNACGRPGGTAVY 350
RESULT 8
IMH1_YEAST
ID IMH1_YEAST STANDARD; PRT; 523 AA.
AC P38697;
IMH3_CANAL
ID IMH3_CANAL STANDARD; PRT; 521 AA.
AC O00086;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN IMH3.
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=3476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SS;
RX MEDLINE=97234646; PubMed=9079920;
RA Koehler G.A., White T.C., Agabian N.;
RT "overexpression of a cloned IMP dehydrogenase gene of Candida
RT albicans confers resistance to the specific inhibitor mycophenolic
RT acid.";
RL J. Bacteriol. 179:2331-2338(1997).
CC -1- FUNCTION: ESSENTIAL ENZYME IN THE DE NOVO BIOSYNTHESIS OF GMP,
CC CATALYSING THE NAD-DEPENDENT OXIDATION OF IMP TO XMP.
CC -1- CATALYTIC ACTIVITY: inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT EQUAL LEVELS IN THE YEAST OR
CC HYPHAL FORM.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL; U85049; AAB51509.1; -.
DR HSSP; P12268; LB30.
DR COMPLEYEST-2DPAGE; O00086; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain. 117 172 CBS 1.
FT DOMAIN 180 232 CBS 2.
FT BINDING 333 333 IMP (POTENTIAL).
FT SEQUENCE 521 AA; 56239 MW; 5F1E52611B1E1418 CRC64;
SQ
Query Match 5.5%; Score 21; DB 1; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 GSICITQEVNACGRPGGTAVY 218
Db 330 GSICITQEVNACGRPGGTAVY 350
RESULT 9
IMH2_YEAST
ID IMH2_YEAST STANDARD; PRT; 523 AA.
AC P50095;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN PUR5 OR YHR216W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetales; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=94378003; PubMed=8091229;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
RA Vignati D., Willcox L., Wohldman P., Waterston R., Wilson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII.";
RL Science 265:2077-2082(1994).
CC -1- CATALYTIC ACTIVITY: inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL; U00029; AAB69728.1; -.
DR PIR; S48997; S48997.
DR HSSP; P12268; LB30.
DR SGD; S0001259; PUR5.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis;
KW Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT DOMAIN 182 234 CBS 2.
FT BINDING 335 335 IMP (POTENTIAL).
FT SEQUENCE 523 AA; 56530 MW; 7CA3EC11238906B9 CRC64;
SQ
Query Match 5.5%; Score 21; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 198 GSICITQEVNACGRPGGTAVY 218
Db 332 GSICITQEVNACGRPGGTAVY 352
RESULT 9
IMH2_YEAST
ID IMH2_YEAST STANDARD; PRT; 523 AA.
AC P50095;
DT 01-OCT-1996 (Rel. 34, Created)
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DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
 DE dehydrogenase) (IMPDH) (IMPD).
 GN YLR432W OR L9753.4.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J.,
 RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
 RA Johnson D., Johnston L., Langston Y., Letreille P., Le T.,
 RA Mardis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D.,
 RA Rifken L., Riles L., Taich A., Trevaskis E., Vignati D.,
 RA Wilcox L., Wohlman P., Vaudin M., Wilson R., Waterston R.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 CC -----
 DR EMBL; U21094; AAB67516.1; -;
 DR HSSP; P12268; 1B30.
 DR SGD; S0004424; YLR432W.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN_enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
 KW Purine biosynthesis; Multigene family; Repeat; CBS domain.
 FT DOMAIN 119 174 CBS 1.
 FT BINDING 182 234 CBS 2.
 FT BINDING 335 335 IMP (POTENTIAL).
 SQ SEQUENCE 523 AA; 56584 MW; A0C84C22527AAE6 CRC64;

 Query Match 5.5%; Score 21; DB 1; Length 523;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 198 GSICITQEVMACGRPGQTAVY 218
 Db 332 GSICITQEVMACGRPGQTAVY 352
 ||||||||||||||||||
 RESULT 10
 IMH3_YEAST
 ID IMH3_YEAST STANDARD; PRT; 524 AA.
 AC P50094;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
 DE dehydrogenase) (IMPDH) (IMPD).
 GN YML056C OR YM9958.06C.

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Devlin K., Churcher C., Barrell B.G., Rajandream M.A.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
 CC xanthosine 5'-phosphate + NADH.
 CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
 CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
 CC GMP REDUCTASE.
 CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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 CC -----
 DR EMBL; Z46729; CAA86719.1; -;
 DR HSSP; P12268; 1B30.
 DR SGD; S0004520; YML056C.
 DR InterPro; IPR000644; CBS.
 DR InterPro; IPR003009; FMN_enzyme.
 DR InterPro; IPR001093; IMP_DH_GMP_RED.
 DR Pfam; PF00571; CBS; 2.
 DR Pfam; PF00478; IMPDH_C; 1.
 DR Pfam; PF01574; IMPDH_N; 1.
 DR SMART; SM00116; CBS; 2.
 DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
 KW Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
 KW Purine biosynthesis; Multigene family; Repeat; CBS domain.
 FT DOMAIN 120 175 CBS 1.
 FT BINDING 183 235 CBS 2.
 FT BINDING 336 336 IMP (POTENTIAL).
 SQ SEQUENCE 524 AA; 56394 MW; A73D1E4EFE8AEAD9 CRC64;

 Query Match 5.5%; Score 21; DB 1; Length 524;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 198 GSICITQEVMACGRPGQTAVY 218
 Db 333 GSICITQEVMACGRPGQTAVY 353
 ||||||||||||||||||
 RESULT 11
 IMDH_LEIDO
 ID IMDH_LEIDO STANDARD; PRT; 514 AA.
 AC P21620;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
 DE dehydrogenase) (IMPDH) (IMPD).
 OS Leishmania donovani.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OX NCBI_TaxID=5661;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91107664; PubMed=1671039;
 RA Wilson K.E., Collart F.R., Huberman E., Stringer J.R., Ullman B.;
 RT "Amplification and molecular cloning of the IMP dehydrogenase gene of
 RT Leishmania donovani."
 RL J. Biol. Chem. 266:1665-1671(1991).
 CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
 CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION


```

CC OF CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M55667; AAA29253.1; -
CC PIR: A38668; A38668.
CC HSSP: P12268; IB30.
CC InterPro: IPR000644; CBS.
CC InterPro: IPR001093; IMP_DH_GMP_RED.
CC Pfam: PF00571; CBS; 2.
CC Pfam: PF00478; IMPDH_C; 1.
CC Pfam: PF01574; IMPDH_N; 1.
CC SMART: SM00116; CBS; 2.
CC PROSITE: PS00487; IMP_DH_GMP_RED; 1.
CC Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
CC CBS domain.
CC KW CBS domain.
CC FT DOMAIN 110 165 CBS 1.
CC FT DOMAIN 172 228 CBS 2.
CC FT BINDING 327 327 IMP (POTENTIAL).
CC FT BINDING 327 327 IMP (POTENTIAL).
CC SEQUENCE 514 AA; 55551 MW; E251FCC1362D60E5 CRC64;

Query Match 3.6%; Score 14; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 ACGRPGGTAVYKVA 221
DB 334 ACGRPGGTAVYKVA 347
|||||
|||||

RESULT 12
IMH4_YEAST
ID IMH4_YEAST STANDARD; PRT; 403 AA.
AC P39567;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN YAR073W OR FUN63.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=95249563; PubMed=7731988;
RA Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
RA Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
RA Storms R.K.;
RT "The nucleotide sequence of chromosome I from Saccharomyces
RT cerevisiae."
RL Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.

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CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L28920; AAC09509.1; -
CC HSSP: P12268; IB30.
CC SGD: S0000095; YAR073W.
CC InterPro: IPR000644; CBS.
CC InterPro: IPR001093; IMP_DH_GMP_RED.
CC Pfam: PF00571; CBS; 2.
CC Pfam: PF00478; IMPDH_C; 1.
CC Pfam: PF01574; IMPDH_N; 1.
CC SMART: SM00116; CBS; 2.
CC PROSITE: PS00487; IMP_DH_GMP_RED; 1.
CC Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
CC Purine biosynthesis; Multigene family; Repeat; CBS domain.
CC KW Purine biosynthesis; Multigene family; Repeat; CBS domain.
CC FT DOMAIN 119 174 CBS 1.
CC FT DOMAIN 182 235 CBS 2.
CC FT BINDING 335 335 IMP (POTENTIAL).
CC SEQUENCE 403 AA; 44386 MW; FEBC13E46D5D1ECD CRC64;

Query Match 3.4%; Score 13; DB 1; Length 403;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 VMACGRPGGTAVY 218
DB 340 VMACGRPGGTAVY 352
|||||
|||||

RESULT 13
IMH2_ARATH
ID IMH2_ARATH STANDARD; PRT; 502 AA.
AC Q9SA34;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN AT1G16350 OR F309.15.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo H., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y., L.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Miltscher J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis

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RT thaliana.";
RL Nature 408:816-820(2000).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 1 CBS DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AC006341; AAD34687.1; -.
CC HSP; P12268; IBS30.
CC InterPro; IPR000644; CBS.
CC InterPro; IPR003009; FMN_enzyme.
CC InterPro; IPR001093; IMP_DH_GMP_RED.
CC Pfam; PF00571; CBS; 1.
CC Pfam; PF00478; IMPDH_C; 1.
CC Pfam; PF01574; IMPDH_N; 1.
CC PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
FT CBS domain. 167 219
FT BINDING 321 322 IMP (POTENTIAL).
SQ SEQUENCE 502 AA; 54051 MW; FB87D84160818310 CRC64;

Query Match 2.9%; Score 11; DB 1; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGVDGLRVGMG 196
DB 306 AGVDGLRVGMG 316
|||||
306 AGVDGLRVGMG 316

RESULT 14
IMH1_ARATH
ID IMH1_ARATH STANDARD; PRT; 503 AA.
AC P47996;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN IMPDH OR AT1G79470 OR T8K14.11.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=97045815; PubMed=8990737;
RA Collart F.R., Osipiuk J., Trent J., Olsen G.J., Huberman E.;
RT "Cloning and characterization of the gene encoding IMP dehydrogenase
RT from Arabidopsis thaliana.";
RL Gene 174:217-220(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,

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RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.-Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.-X., Liu Z.A., Luros J.S., Malti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
CC EMBL; L34684; AAB41940.1; -.
CC EMBL; AC007202; AAD30229.1; -.
CC HSP; P12268; IBS30.
CC InterPro; IPR000644; CBS.
CC InterPro; IPR003009; FMN_enzyme.
CC InterPro; IPR001093; IMP_DH_GMP_RED.
CC Pfam; PF00571; CBS; 1.
CC Pfam; PF00478; IMPDH_C; 1.
CC Pfam; PF01574; IMPDH_N; 1.
CC PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
FT CBS domain. 322 322 IMP (POTENTIAL).
SQ SEQUENCE 503 AA; 54194 MW; ADDDAF9C3A697A9A CRC64;

Query Match 2.9%; Score 11; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGVDGLRVGMG 196
DB 307 AGVDGLRVGMG 317
|||||
307 AGVDGLRVGMG 317

RESULT 15
IMDH_PNECA
ID IMDH_PNECA STANDARD; PRT; 454 AA.
AC Q12658;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GUAL.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97135213; PubMed=8980752;
RA O'Gara M.J., Lee C.H., Weinberg G.A., Nott J.M., Queener S.F.;

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RT *IMP dehydrogenase from Pneumocystis carinii as a potential drug
RL target.
RL Antimicrob. Agents Chemother. 41:40-48(1997).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL; U42442; AAA97462.1; -.
DR HSSP; P12268; 1B30.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain.
FT DOMAIN 47 102 CBS 1.
FT DOMAIN 109 163 CBS 2.
FT BINDING 263 263 IMP (BY SIMILARITY).
SQ SEQUENCE 454 AA; 49522 MW; 5E4B64426A730947 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 454;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTE 75
Db |||||
2 SSPMDTVTE 10

RESULT 16
IMDH_METJA STANDARD; PRT; 496 AA.
AC Q59011;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GUAB OR MJ1616.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Peter M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";

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RL Science 273:1058-1073(1996).
CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL; U67602; AAB99638.1; -.
DR HSSP; P12268; 1B30.
DR TIGR; MJ1616; -.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT DOMAIN 43 95 CBS 1.
FT BINDING 103 155 CBS 2.
FT BINDING 306 306 IMP (POTENTIAL).
SQ SEQUENCE 496 AA; 53316 MW; C3E03FDDF3898396 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 496;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 VPIIADGGI 237
Db |||||
334 VPIIADGGI 342

RESULT 17
IMDH_TRYBB STANDARD; PRT; 512 AA.
AC P50098;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
OS Trypanosoma brucei brucei.
OC Eukaryota; Eucleozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EATRO 164 / ISTAT 1.7;
RX MEDLINE=95050714; PubMed=7961861;
RA Wilson K., Berens R.L., Sifri C.D., Ullman B.;
RT "Amplification of the inosinate dehydrogenase gene in Trypanosoma
brucei gambiense due to an increase in chromosome copy number.";
RL J. Biol. Chem. 269:28979-28987(1994).
CC -!- FUNCTION: IMP IS THE RATE LIMITING ENZYME IN THE DE NOVO SYNTHESIS
CC OF GUANINE NUCLEOTIDES AND THEREFORE IS INVOLVED IN THE REGULATION
CC OF CELL GROWTH.
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -----

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CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL; M97794; AAB46420.1; -;
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain.
FT DOMAIN 108 163 CBS 1.
FT DOMAIN 170 226 CBS 2.
FT BINDING 325 325 IMP (POTENTIAL).
SQ SEQUENCE 512 AA; 55708 MW; 1A86C46AE6445045 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 512;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTE 75
Db 63 SSPMDTVTE 71
| | | | | | | | | |

RESULT 18
POLY_DROME STANDARD; PRT; 1035 AA.
AC P10401; P10402;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Retrovirus-related POL polyprotein from transposon gypsy [Contains:
DE Reverse transcriptase (EC 2.7.7.49); Endonuclease].
GN POL.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87064379; PubMed=3023871;
RA Marlor R.L., Parkhurst S.M., Corces V.G.;
RT "The Drosophila melanogaster gypsy transposable element encodes
RT putative gene products homologous to retroviral proteins.";
RL Mol. Cell. Biol. 6:1129-1134(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92293139; PubMed=1318501;
RA Smith P.A., Corces V.G.;
RT "The suppressor of hairy-wing binding region is required for gypsy
RT mutagenesis.";
RL Mol. Gen. Genet. 233:65-70(1992).
RN [3]
RP SEQUENCE OF 21-950 FROM N.A.
RX MEDLINE=86176782; PubMed=2421255;
RA Yuki S., Ishimaru S., Inouye S., Saigo K.;
RT "Identification of genes for reverse transcriptase-like enzymes in

RT two Drosophila retrotransposons, 412 and gypsy; a rapid detection
RT method of reverse transcriptase genes using YXDD box probes.";
RL Nucleic Acids Res. 14:3017-3030(1986).
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CC -----
DR EMBL; M12927; AAA70219.1; ALT_INIT.
DR EMBL; X03734; CAA27371.1; -;
DR PIR; B25666; GNFEGL.
DR HSSP; P03366; LHMV.
DR Flybase; FBgn0014966; gypsy/pol.
DR InterPro; IPR001995; Asp_prot_retrov.
DR InterPro; IPR000477; RVTse.
DR InterPro; IPR001584; Rve.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; kvp; 1.
DR Pfam; PF00078; rvt; 1.
KW Hydrolase; Endonuclease; Transferase; RNA-directed DNA polymerase;
KW Polyprotein; Transposable element.
FT CONFLICT 31 32 DA -> AR (IN REF. 3).
FT CONFLICT 60 60 G -> R (IN REF. 3).
FT CONFLICT 232 232 F -> S (IN REF. 3).
FT CONFLICT 490 490 D -> V (IN REF. 3).
FT CONFLICT 883 883 S -> T (IN REF. 3).
FT CONFLICT 923 923 N -> S (IN REF. 3).
FT CONFLICT 947 950 RPIE -> NOLR (IN REF. 3).
SQ SEQUENCE 1035 AA; 117818 MW; 7B985CA272B8A5A6 CRC64;

Query Match 2.3%; Score 9; DB 1; Length 1035;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LDLLTQAGV 138
Db 94 LDLLTQAGV 102
| | | | | | | | | |

RESULT 19
RS17_CHLPN STANDARD; PRT; 86 AA.
AC Q927R6; Q9JQ66;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30S ribosomal protein S17.
GN RPSQ OR RS17 OR CPN0638 OR CP0109.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE=99208606; PubMed=10192388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AR39;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Baas S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;

RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
 RL pneumoniae AR39.";
 CC Nucleic Acids Res. 28:1397-1406(2000).
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN-J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).

CC -1- FUNCTION: PROTEIN S17 BINDS SPECIFICALLY TO THE 5' END OF 16S
 CC RIBOSOMAL RNA (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE S17P FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL; AE001647; AAD18777.1; -;
 DR EMBL; AF002173; AAF37992.1; -;
 DR EMBL; AF002547; BAA98845.1; -;
 DR HSSP; P23828; 1RIP.
 DR TIGR; CP0109; -;

DR InterPro: IPR000266; Ribosomal_S17.
 DR Pfam; PF00366; Ribosomal_S17; 1.
 DR PRINTS; PR00973; RIBOSOMALS17.
 DR PRODOM; PD001295; Ribosomal_S17; 1.
 DR PROSITE; PS00056; RIBOSOMAL_S17; 1.

DR KW Ribosomal protein; rRNA-binding; Complete proteome.
 SQ SEQUENCE 86 AA; 9889 MW; 7EA25422922FC114 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 86;

Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 SEGDKVKI 309

|||||||

Db 57 SEGDKVKI 64

RESULT 20

YC43_PORPU

ID YC43_PORPU STANDARD; PRT; 254 AA.

AC P51264;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 28.1 kDa protein ycf43 (ORF254).

GN Ycf43.

OS Porphyra purpurea.

OG Chloroplast.

OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Porphyra.

OX NCBI_TaxID=2787;

RN [1]

SEQUENCE FROM N.A.

RP STRAIN=AVONPORT;

RA Reith M.E., Munholland J.;

RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast

genome.";

RL Plant Mol. Biol. Rep. 13:333-335(1995).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- SIMILARITY: BELONGS TO THE TATC FAMILY.

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 CC -----

DR EMBL; U38804; AAC08150.1; -;
 DR Mendel; I0389; PORPU:ycf43; 1.
 DR InterPro: IPR002033; UPF0032.
 DR Pfam; PF00902; UPF0032; 1.
 DR PROSITE; PS01218; TATC; 1.

KW Chloroplast; Hypothetical protein; Transmembrane.

FT TRANSMEM 41 61 POTENTIAL.

FT TRANSMEM 64 84 POTENTIAL.

FT TRANSMEM 91 111 POTENTIAL.

FT TRANSMEM 125 145 POTENTIAL.

FT TRANSMEM 146 166 POTENTIAL.

FT TRANSMEM 172 192 POTENTIAL.

FT TRANSMEM 204 224 POTENTIAL.

FT TRANSMEM 232 252 POTENTIAL.

SQ SEQUENCE 254 AA; 28149 MW; EE297AE89731AE11 CRC64;

Query Match

2.1%; Score 8; DB 1; Length 254;

Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 266 APGEYEFS 273

|||||||

Db 78 APGEYEFS 85

RESULT 21

GOX1_ARATH

ID GOX1_ARATH STANDARD; PRT; 367 AA.

AC Q9LR80;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable (S)-2-hydroxy-acid oxidase, peroxisomal 1 (EC 1.1.3.15)

DE (Glycolate oxidase 1) (GOX 1) (Short chain alpha-hydroxy acid oxidase

1).

GN AT3G14415 OR MLN21.20.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RX MEDLINE=20277480; PubMed=10819329;

RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence

features of the regions of 4,504,864 bp covered by sixty P1 and TAC

clones.";

RL DNA Res. 7:131-135(2000).

CC -1- CATALYTIC ACTIVITY: (S)-2-hydroxy-acid + O(2) = 2-oxo acid +

H(2)O(2).

CC -1- COFACTOR: FMN (BY SIMILARITY).

CC -1- PATHWAY: SECOND REACTION OF THE PHOTORESPIRATORY PATHWAY

CC (GLYCOLATE PATHWAY).

CC -1- SUBUNIT: HOMOTETRAMER OR HOMOOCTAMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Peroxisomal (By similarity).

CC -1- SIMILARITY: BELONGS TO THE FMN-DEPENDENT ALPHA-HYDROXY ACID

DEHYDROGENASES FAMILY.

CC -----

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 CC -----

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CC -----
DR EMBL; AB028617; BAB01333.1; -.
DR EMBL; AB022220; BAB01333.1; JOINED.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR000262; FMN_hydroxy_acid_dh.
DR Pfam; PF01070; FMN_dh; 1.
DR PROSITE; PS00342; MICROBODIES_C; 1.
DR Oxidoreductase; Flavoprotein; FMN; Peroxisome; Glycolate pathway;
KW Photorespiration.
DR ACT_SITE 24 24 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 129 129 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 254 254 REMOVES THE SUBSTRATE ALPHA-PROTON AS THE
FT FIRST STEP IN CATALYSIS (BY SIMILARITY).
FT ACT_SITE 257 257 SUBSTRATE BINDING (BY SIMILARITY).
FT SITE 365 367 MICROBODY TARGETING SIGNAL (POTENTIAL).
SQ SEQUENCE 367 AA; 40306 MW; C0H0F9B083F1B6E6 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 KALALGAS 252
DB 296 KALALGAS 303
|||||

RESULT 22
GOX2_ARATH STANDARD; PRT; 367 AA.
AC Q9LRR9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable (S)-2-hydroxy-acid oxidase, peroxisomal 2 (EC 1.1.3.15)
DE (Glycolate oxidase 2) (GOX 2) (Short chain alpha-hydroxy acid oxidase
DE 2).
GN AT3G14420 OR MAO2.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asanizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones";
RL DNA Res. 7:131-135(2000).
CC -!- CATALYTIC ACTIVITY: (S)-2-hydroxy-acid + O(2) -> 2-oxo acid +
CC H(2)O(2).
CC -!- COFACTOR: FMN (BY SIMILARITY).
CC -!- PATHWAY: SECOND REACTION OF THE PHOTORESPIRATORY PATHWAY
CC (GLYCOLATE PATHWAY).
CC -!- SUBUNIT: HOMOTETRAMER OR HOMOOCTAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Peroxisomal (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FMN-DEPENDENT ALPHA-HYDROXY ACID
CC DEHYDROGENASES FAMILY.
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CC -----
DR EMBL; AB028617; BAB01334.1; -.

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DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR000262; FMN_hydroxy_acid_dh.
DR Pfam; PF01070; FMN_dh; 1.
DR PROSITE; PS00342; MICROBODIES_CTER; 1.
DR Oxidoreductase; Flavoprotein; FMN; Peroxisome; Glycolate pathway;
KW Photorespiration.
DR ACT_SITE 24 24 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 129 129 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 254 254 REMOVES THE SUBSTRATE ALPHA-PROTON AS THE
FT FIRST STEP IN CATALYSIS (BY SIMILARITY).
FT ACT_SITE 257 257 SUBSTRATE BINDING (BY SIMILARITY).
FT SITE 365 367 MICROBODY TARGETING SIGNAL (POTENTIAL).
SQ SEQUENCE 367 AA; 40341 MW; B107AD7AC983A04C CRC64;

Query Match 2.1%; Score 8; DB 1; Length 367;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 KALALGAS 252
DB 296 KALALGAS 303
|||||

RESULT 23
Y165_RICPR STANDARD; PRT; 368 AA.
AC Q92D28;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein Rpl65.
GN Rpl65.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria";
RL Nature 396:133-140(1998).
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CC -----
DR EMBL; AJ235270; CAJ14632.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 368 AA; 41009 MW; 0410168F891F489C CRC64;

Query Match 2.1%; Score 8; DB 1; Length 368;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 AVYKVAEY 223
DB 256 AVYKVAEY 263
|||||

RESULT 24
MDLB_PSEPU

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ID MDLB_PSEPU STANDARD; PRT; 393 AA.
AC P20932;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE L(+)-mandelate dehydrogenase (EC 1.1.1.-) (S-mandelate dehydrogenase)
DE (MDH).
DE MDLB.
GN Pseudomonas putida.
OS Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-30.
RC STRAIN=APCC 12633;
RX MEDLINE=91104894; PubMed=2271624;
RA TSOU A.Y., Ransom S.C., Gerlt J.A., Buechter D.D., Babbitt P.C.,
Kenyon G.L.;
RT "Mandelate pathway of Pseudomonas putida: sequence relationships
involving mandelate racemase, (S)-mandelate dehydrogenase, and
benzoylformate decarboxylase and expression of benzoylformate
decarboxylase in Escherichia coli.";
RL Biochemistry 29:9856-9862(1990).
CC -1- FUNCTION: REDUCTION OF L(+)-MANDELATE TO BENZOYLFORMATE.
CC -1- COFACTOR: FMN.
CC -1- PATHWAY: MANDELATE PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE FMN-DEPENDENT ALPHA-HYDROXY ACID
DEHYDROGENASES FAMILY.
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-----
DR EMBL; J05293; AAC15503.1; -.
DR PIR; B47767; B44767.
DR HSSP; P05414; 1G0X.
DR InterPro; IPR003109; FMN-enzyme.
DR InterPro; IPR000262; FMN_hydroxy_acid_dh.
DR Pfam; PF01070; FMN_dh; 1.
DR PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.
DR Oxidoreductase; Mandelate pathway; Aromatic hydrocarbons catabolism;
KW Flavoprotein; FMN.
FT ACT_SITE 26 26 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 131 131 SUBSTRATE BINDING (BY SIMILARITY).
FT ACT_SITE 274 274 REMOVES THE SUBSTRATE ALPHA-PROTON AS THE
FIRST STEP IN CATALYSIS (BY SIMILARITY).
FT ACT_SITE 277 277 SUBSTRATE BINDING (BY SIMILARITY).
SQ SEQUENCE 393 AA; 43437 MW; 18BE23B459BB3987 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 393;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 VKALALGA 251
Db 313 VKALALGA 320
|||||||

RESULT 25
IMDH_HELPJ STANDARD; PRT; 481 AA.
AC Q9ZLL4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPD).
GN GUAB OR JHP0768.

ID IMDH_HELPJ STANDARD; PRT; 481 AA.
AC P56088;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPD).
GN GUAB OR HP0829.

OS Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]

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OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir B.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
gastric pathogen Helicobacter pylori.";
RL Nature 397:176-180(1999).
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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DR EMBL; AE001507; AAD06347.1; -.
DR HSSP; P49058; 1EEP.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN-enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT DOMAIN 89 142 CBS 1.
FT DOMAIN 150 204 CBS 2.
FT BINDING 300 300 IMP (POTENTIAL).
SQ SEQUENCE 481 AA; 51688 MW; 688262DCD14EFDAB CRC64;

Query Match 2.1%; Score 8; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
Db 344 KALALGAS 351
|||||||

RESULT 26
IMDH_HELPY STANDARD; PRT; 481 AA.
AC P56088;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
dehydrogenase) (IMPDH) (IMPD).
GN GUAB OR HP0829.
OS Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]

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RP SEQUENCE FROM N.A.
RX STRAIN=26695 / ATCC 700392;
RC MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Kar P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547(1997).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL; AE000594; AAC07879.1; -.
DR HSSP; P49058; 1EEP.
DR TIGR; HP0829; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT DOMAIN 89 142 CBS 1.
FT DOMAIN 150 204 CBS 2.
FT BINDING 300 300 IMP (POTENTIAL).
FT BINDING 481 AA; 51802 MW; 075A84B1F8AC9481 CRC64;
SQ SEQUENCE 481 AA; 51802 MW; 075A84B1F8AC9481 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 481;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
DB 344 KALALGAS 351
|||||||

RESULT 27
IMDH_AQUAE STANDARD; PRT; 490 AA.
AC O67820;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GUAB OR AQ.2023.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]

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RP SEQUENCE FROM N.A.
RX STRAIN=VF5;
RC MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.B., Overbeek R., Shead M.A., Keller M., Aujaay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -!- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -!- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -!- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL; AE000768; AAC07779.1; -.
DR HSSP; P50099; 1ZPJ.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
DR Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
KW CBS domain; Complete proteome.
FT DOMAIN 93 146 CBS 1.
FT DOMAIN 156 210 CBS 2.
FT BINDING 309 309 IMP (POTENTIAL).
FT BINDING 490 AA; 53400 MW; 66605CDD8B348CE4 CRC64;
SQ SEQUENCE 490 AA; 53400 MW; 66605CDD8B348CE4 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 490;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237
DB 338 PIIADGGI 345
|||||||

RESULT 28
IMDH_RHTR STANDARD; PRT; 498 AA.
AC Q9KH33;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
GN GUAB.
OS Rhizobium tropici.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=398;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=899;
RA Riccillo P.M., Collavino M.M., Grasso D.H., England R.,
RA de Bruijn F.J., Aguilar M.;
RT "Guab from Rhizobium tropici 899.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =

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CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC
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CC
CC -----
CC EMBL: AF272827; AAF85967.1; -.
CC DR InterPro: IPR000644; CBS.
CC DR InterPro: IPR003009; FMN_enzyme.
CC DR InterPro: IPR001093; IMP_DH_GMP_RED.
CC DR Pfam: PF00571; CBS; 2.
CC DR Pfam: PF00478; IMPDH_C; 1.
CC DR Pfam: PF01574; IMPDH_N; 1.
CC DR SMART: SM00116; CBS; 2.
CC DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
CC KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
CC KW CBS domain.
CC FT DOMAIN 96 150 CBS 1.
CC FT DOMAIN 158 211 CBS 2.
CC FT BINDING 310 310 IMP (POTENTIAL).
CC SQ SEQUENCE 498 AA; 52835 MW; 0A99E38B1078ED73 CRC64;

Query Match 2.1%; Score 8; DB 1; Length 498;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237
DB 339 PIIADGGI 346

RESULT 29
ID IMDH_CHLVI STANDARD; PRT; 521 AA.
AC G50316;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) (IMP
DE dehydrogenase) (IMPDH) (IMPD).
DE GUAB.
GN Chlorobium vibrioforme.
OS Bacteria; Green sulfur bacteria; Chlorobium.
OC NCBI_TaxID=1098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F. THIOSULFATOPHILUM NCIB 8327;
RA Petersen B.L., Moeller M.G., Stummann B.M., Henningsen K.W.;
RT "Clustering of genes with function in the biosynthesis of
RT bacteriochlorophyll and heme in the green sulfur bacterium Chlorobium
RT vibrioforme."
RL Hereditas 125:93-96(1996).
CC
CC -1- CATALYTIC ACTIVITY: Inosine 5'-phosphate + NAD(+) + H(2)O =
CC xanthosine 5'-phosphate + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC
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CC
CC -----
CC EMBL: Z83933; CAB06303.1; -.
CC DR HSSP: P49058; IEEP.
CC DR InterPro: IPR000644; CBS.
CC DR InterPro: IPR003009; FMN_enzyme.
CC DR InterPro: IPR001093; IMP_DH_GMP_RED.
CC DR Pfam: PF00571; CBS; 2.
CC DR Pfam: PF00478; IMPDH_C; 1.
CC DR Pfam: PF01574; IMPDH_N; 1.
CC DR SMART: SM00116; CBS; 2.
CC DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
CC KW Oxidoreductase; NAD; GMP biosynthesis; Purine biosynthesis; Repeat;
CC KW CBS domain.
CC FT DOMAIN 118 176 CBS 1.
CC FT DOMAIN 184 237 CBS 2.
CC FT BINDING 336 336 IMP (POTENTIAL).
CC SQ SEQUENCE 521 AA; 56627 MW; 0065FCCBC182815A CRC64;

Query Match 2.1%; Score 8; DB 1; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237
DB 365 PIIADGGI 372

RESULT 30
ID Y22B_HAEIN STANDARD; PRT; 163 AA.
AC O86223;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Very hypothetical protein HI0221.1.
GN HI0221.1.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OC NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd."
RL Science 269:496-512(1995).
RN [2]
RP IDENTIFICATION.
RA White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D., Peterson J.,
RA Hickey E., Dodson R., Gwinn M.;
RA Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE PSEUDOGENE; CORRESPONDS A TANDEM COPY OF THE C-
CC TERMINAL REGION OF GUAB (HI0221).
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO
CC GMP REDUCTASE.
CC
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DR EMBL: U32708; AAC21895.1; -;
 DR HSSP: P50099; 12FJ.
 DR TIGR: HI0221.1; -;
 DR InterPro: IPR001093; IMP_DH_GMP_RED.
 DR Pfam: PF00478; IMPDH_C; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 163 AA; 18406 MW; 04433231582FAC57 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 163;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 YRGMGSL 287
 |||||
 Db 61 YRGMGSL 67

RESULT 31

IF3_XYLFA
 ID IF3_XYLFA STANDARD; PRT; 180 AA.
 AC Q9PFE1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Translation initiation factor IF-3.
 GN INFC OR XF0737.
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9A5C;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.P., Camargo A.E., Camargo L.E.A., Carraro D.M., Carrier H.,
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A., Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quadrio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa";
 RL Nature 406:151-159(2000).
 CC -!- FUNCTION: IF-3 BINDS TO THE 30S RIBOSOMAL SUBUNIT AND SHIFTS THE
 CC EQUILIBRIUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN
 CC FAVOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABILITY OF 30S
 CC SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE IF-3 FAMILY.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE IF-3 FAMILY.
 CC -----

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DR EMBL: AE003916; AAF83547.1; ALT_INIT.
 DR InterPro: IPR001288; IF3.
 DR Pfam: PF00707; IF3; 1.
 DR ProDom: PD002880; IF3; 1.
 DR PROSITE: PS00938; IF3; 1.
 KW Initiation factor; Protein biosynthesis; Complete proteome.
 SQ SEQUENCE 180 AA; 20831 MW; 95F86FB9C1EF76 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 180;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 EGDVKVI 309
 |||||
 Db 121 EGDVKVI 127

RESULT 32

IF3_RHOSH
 ID IF3_RHOSH STANDARD; PRT; 181 AA.
 AC Q33567;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Translation initiation factor IF-3.
 GN INFC OR PIFC.
 OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Rhodobacter.
 OX NCBI_TaxID=1063;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
 RX MEDLINE=98036135; PubMed=9370368;
 RA Babic S., Hunter C.N., Rakhlin N.J., Simons R.W., Phillips-Jones M.K.;
 RT "Molecular characterisation of the pifc gene encoding translation
 RT initiation factor 3, which is required for normal photosynthetic
 RT complex formation in Rhodobacter sphaeroides NCIB 8253";
 RL Eur. J. Biochem. 249:564-575(1997).
 CC -!- FUNCTION: IF-3 BINDS TO THE 30S RIBOSOMAL SUBUNIT AND SHIFTS THE
 CC EQUILIBRIUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN
 CC FAVOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABILITY OF 30S
 CC SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE IF-3 FAMILY.
 CC -----

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DR EMBL: Y14733; CAA75028.1; -;
 DR HSSP: P02999; 2IFE.
 DR InterPro: IPR001288; IF3.
 DR Pfam: PF00707; IF3; 1.
 DR ProDom: PD002880; IF3; 1.
 DR PROSITE: PS00938; IF3; 1.

KW Initiation factor; Protein biosynthesis.
SQ SEQUENCE 181 AA; 20541 MW; 36B720F3BB21BEF4 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 SEGDKVK 308
|||||||
DB 122 SEGDKVK 128

RESULT 33

PP1A_PSEAE STANDARD; PRT; 187 AA.
AC Q59641; Q9HZ13;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Peptidyl-prolyl cis-trans isomerase A precursor (EC 5.2.1.8) (PPIase
A) (Rotamase A) (Cyclophilin A).
GN PP1A OR CYPH OR PA3227.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzer L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RN [2]
RP SEQUENCE OF 22-175 FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=96146052; PubMed=8581173;
RA Liao X., Charlebois I., Ouellet C., Morency M.J., Dewar K.,
RA Lightfoot J., Foster J., Siehnell R., Schweizer H., Lam J.S.,
RA Hancock R.E., Levesque R.C.;
RT "Physical mapping of 32 genetic markers on the Pseudomonas aeruginosa
RT PA01 chromosome.";
RL Microbiology 142:79-86(1996).
CC -1- FUNCTION: PPIASES ACCELERATE THE FOLDING OF PROTEINS. THIS PROTEIN
CC IS NOT ESSENTIAL FOR GROWTH. PRESUMABLY A ROLE IN SIGNAL
CC TRANSDUCTION.
CC -1- CATALYTIC ACTIVITY: CIS-TRANS ISOMERIZATION OF PROLINE IMIDIC
CC PEPTIDE BONDS IN OLIGOPETIDES.
CC -1- SUBCELLULAR LOCATION: Periplasmic (Probable).
CC -1- SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
CC -----
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CC -----
DR EMBL; AF004745; AAC06615.1; -;
DR EMBL; X84050; CAA58868.1; -;
DR HSSP; P20752; 1CLH.
DR InterPro; IPR002130; CSA_PPIase.
DR Pfam; PF00160; pro_isomerase; 1.
DR PRINTS; PR00153; CSAPPISMRASE.
DR PROSITE; PS00170; CSA_PPIASE_1; FALSE_NEG.

DR PROSITE; PS0072; CSA_PPIASE_2; 1.
KW Isomerase; Rotamase; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 187 PSPTIDYL-PROLYL CIS-TRANS ISOMERASE A.
FT CONFLICT 22 24 TPA -> GTT (IN REF. 2).
FT CONFLICT 173 174 DV -> SL (IN REF. 2).
SQ SEQUENCE 187 AA; 20104 MW; 5664DBC83FB94594 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 187;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 GSLLAAT 263
|||||||
DB 16 GSLLAAT 22

RESULT 34

YBF9_YEAST STANDARD; PRT; 193 AA.
AC P34224;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 22.3 kDa protein in SKT5-SHP1 intergenic region.
GN YBL059W OR YBL0508 OR YBL0516.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94205266; PubMed=8154187;
RA Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.;
RT "Sequencing and functional analysis of a 32,560 bp segment on the
RT left arm of yeast chromosome II. Identification of 26 open reading
RT frames, including the KIP1 and SEC17 genes.";
RL Yeast 9:1355-1371(1993).
RN [2]
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CC -----
DR EMBL; Z23261; CAA80788.1; -;
DR EMBL; Z35820; CAA84879.1; -;
DR PIR; S39829; S39829.
DR PIR; S37330; S37330.
DR SGD; S0000155; YBL059W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 119 143 POTENTIAL.
SQ SEQUENCE 193 AA; 22278 MW; 891A434C861C1B59 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 GSLLAAT 263
|||||||
DB 121 GSLLAAT 127

RESULT 35

MTR2_MOUSE STANDARD; PRT; 227 AA.
ID MTR2_MOUSE
AC Q92ZD1.
DT 16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Myotubularin-related protein 2 (Fragment).
GN MTWR2.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98409499; PubMed=9736772;
RA Laporte J., Blondeau F., Buj-Bello A., Tentler D., Kretz C., Dahl N.,
RA Mandel J.-L.;
RT "Characterization of the myotubularin dual specificity phosphatase
RT gene family from yeast to human.";
RL Hum. Mol. Genet. 7:1703-1712(1998).
CC -!- FUNCTION: NOT KNOWN, COULD BE A TYROSINE-PHOSPHATASE.
CC -!- SIMILARITY: BELONGS TO THE MYOTUBULARIN-LIKE FAMILY.
CC
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CC
CC EMBL; AF073880; AAC80002.1; -
CC MGD; MGI:1924366; Mmnr2.
CC InterPro; IPR004182; GRAM.
CC InterPro; IPR000387; TYR_phosphatase.
CC Pfam; PF02893; GRAM; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; PARTIAL.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; PARTIAL.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 227 227
SQ SEQUENCE 227 AA; 25201 MW; 71D540D39AD290C6 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 289 AMEKSSS 295
| | | | | | | |
DB 2 AMEKSSS 8

RESULT 36
Y134.METJA
ID Y134.METJA STANDARD; PRT; 282 AA.
AC Q57598;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0134.
GN MJ0134.
OS Methanococcus jannaschii.
CC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
CC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868087;
RA Sult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: LOW, TO YEAST GCD14.
CC
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CC
CC EMBL; U67470; AAB98115.1; -
CC TIGR; MJ0134; -
CC InterPro; IPR001737; RNA_A_dimeth.
CC InterPro; IPR000051; SAM_bind.
CC Pfam; PF00398; RnaAad; 1.
CC Hypothetical protein; Complete proteome.
SQ SEQUENCE 282 AA; 32207 MW; 558FB972B21CFA9C CRC64;

Query Match 1.8%; Score 7; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 VDVIVLD 144
| | | | | | | |
DB 182 VDVIVLD 188

RESULT 37
YEA5.YEAST
ID YEA5.YEAST STANDARD; PRT; 282 AA.
AC P40003;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 31.4 kDa protein in GCNA-WBP1 intergenic region.
GN YEL005C.
OS Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U18530; AAB64482.1; -
CC SGD; S0000731; VAB2.
KW Hypothetical protein.
SQ SEQUENCE 282 AA; 31364 MW; 8F7CA122F91E491A CRC64;

Query Match 1.8%; Score 7; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 42;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 SAGSLTY 32
|||||

Db 264 SAGSLTY 270

RESULT 38

YC43_GUITH STANDARD; PRT; 290 AA.

AC 078493;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical 33.1 kDa protein ycf43.

GN YCF43.

OS Guillardia theta (Cryptomonas phi).

OC Chloroplast.

OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.

OX NCBI_TaxID=55529;

[1]

RN SEQUENCE FROM N.A.

RP MEDLINE=99128221; PubMed=9929392;

RA Douglas S.E., Penny S.L.;

RT complete sequence and conserved syntenic groups confirm its common ancestry with red algae.";

RL J. Mol. Evol. 48:236-244(1999).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- SIMILARITY: BELONGS TO THE TATC FAMILY.

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DR EMBL; AF041468; AAC35684.1; .

DR InterPro: IPR002033; UPF0032.

DR Pfam: PF00902; UPF0032; 1.

DR PROSITE; PS01218; TATC; FALSE_NEG.

KW Chloroplast; Hypothetical protein; Transmembrane.

FT TRANSMEM 71 91 POTENTIAL.

FT TRANSMEM 124 144 POTENTIAL.

FT TRANSMEM 155 175 POTENTIAL.

FT TRANSMEM 202 222 POTENTIAL.

FT TRANSMEM 234 254 POTENTIAL.

FT TRANSMEM 262 282 POTENTIAL.

SQ SEQUENCE 290 AA; 33161 MW; CD637821194FAP2F CRC64;

Query Match 1.8%; Score 7; DB 1; Length 290;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 266 APGEYFF 272

|||||

Db 108 APGEYFF 114

RESULT 39

CD20_HUMAN STANDARD; PRT; 297 AA.

AC P11836; P08984; Q13963;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE B-lymphocyte antigen CD20 (B-lymphocyte surface antigen B1) (Leu-16) (Bp35).

DE B-lymphocyte antigen CD20 (B-lymphocyte surface antigen B1) (Leu-16) (Bp35).

GN MS4A1 OR CD20.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

RN SEQUENCE FROM N.A.

RP MEDLINE=88258386; PubMed=3260267;

RA Stamenkovic I., Seed B.;

RT "Analysis of two cDNA clones encoding the B lymphocyte antigen CD20 (B1, Bp35), a type III integral membrane protein.";

RL J. Exp. Med. 167:1975-1980(1988).

[2]

RN SEQUENCE FROM N.A.

RP MEDLINE=88124792; PubMed=2448768;

RA Tedder T.F., Streuli M., Schlossman S.F., Saito H.;

RT "Isolation and structure of a cDNA encoding the B1 (CD20) cell-surface antigen of human B lymphocytes.";

RL Proc. Natl. Acad. Sci. U.S.A. 85:208-212(1988).

[3]

RN SEQUENCE FROM N.A.

RP MEDLINE=89176281; PubMed=2466899;

RA Tedder T.F., Klejman G., Schlossman S.F., Saito H.;

RT "Structure of the gene encoding the human B lymphocyte differentiation antigen CD20 (B1).";

RL J. Immunol. 142:2560-2568(1989).

[4]

RN SEQUENCE FROM N.A.

RP MEDLINE=88283639; PubMed=2456210;

RA Einfield D.A., Brown J.P., Valentine M.A., Clark E.A., Ledbetter J.A.;

RT "Molecular cloning of the human B cell CD20 receptor predicts a hydrophobic protein with multiple transmembrane domains.";

RL EMBO J. 7:711-717(1988).

CC -!- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE REGULATION OF B-CELL ACTIVATION AND PROLIFERATION.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- PTM: PHOSPHORYLATED. MIGHT BE FUNCTIONALLY REGULATED BY PROTEIN KINASE(S).

CC -!- SIMILARITY: BELONGS TO THE MS4A FAMILY.

CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD20 entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd20.htm".

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DR EMBL; X12530; CAA31046.1; .

DR EMBL; M27394; AAA35581.1; .

DR EMBL; M27395; -; NOT_ANNOTATED_CDS.

DR EMBL; L23419; AAA88911.1; .

DR EMBL; L23415; AAA88911.1; JOINED.

DR EMBL; L23416; AAA88911.1; JOINED.

DR EMBL; L23417; AAA88911.1; JOINED.

DR EMBL; X07203; CAA30179.1; .

DR EMBL; X07204; CAA30180.1; .

DR PIR; A27400; A27400.

DR PIR; JL0042; JL0042.

DR PIR; A30586; A30586.

DR PIR; S00387; S00387.

DR MIM; 112210; .

KW B-cell; Transmembrane; Phosphorylation.

FT DOMAIN 1 63 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 64 84 POTENTIAL.

FT TRANSMEM 85 105 POTENTIAL.

FT TRANSMEM 121 141 POTENTIAL.

FT TRANSMEM 189 209 POTENTIAL.

FT DOMAIN 210 297 CYTOPLASMIC (POTENTIAL).

FT DISULFID 81 167 PROBABLE.

FT DISULFID 167 183 PROBABLE.

FT DISULFID 111 220 PROBABLE.

FT CONFLICT 13 13 P -> L (IN REF. 4).

FT CONFLICT 71 M -> I (IN REF. 3).
SQ SEQUENCE 297 AA: 33077 MW: AC5420F8B626BDD1 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 GSLLAAT 263
|||||||
DB 98 GSLLAAT 104

RESULT 40

PYRD_METJA STANDARD; PRT; 306 AA.
AC Q58070;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dihydroorotate dehydrogenase (EC 1.3.3.1) (Dihydroorotate oxidase)
DE (DHodehase) (DHODase) (DHOD).
GN PYRD OR MJ0654.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii".
RL Science 273:1058-1073(1996).
CC -!- CATALYTIC ACTIVITY: (S)-dihydroorotate + O(2) = orotate +
CC H(2)O(2).
CC -!- COFACTOR: FMN (BY SIMILARITY).
CC -!- PATHWAY: FOURTH STEP IN PYRIMIDINE BIOSYNTHESIS.
CC -!- SUBUNIT: HETEROTETRAMER OF 2 PYRD AND 2 PYRD SUBUNITS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE DIHYDROOROTATE DEHYDROGENASE FAMILY.
CC SUBFAMILY 1.

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DR EMBL; U67513; AAB98649.1; -.
DR HSP; P54321; 2DOR.
DR TIGR; MJ0654; -.
DR InterPro; IPR001295; DHO_dh.
DR InterPro; IPR003009; FMN_enzyme.
DR Pfam; PF01180; DHodehase; 1.
DR PROSITE; PS00911; DHODEHASE_1; 1.
DR PROSITE; PS00912; DHODEHASE_2; 1.
KW Pyrimidine biosynthesis; Oxidoreductase; Flavoprotein; FMN;
KW Complete proteome.
FT NP_BIND 240 248 FMN (POTENTIAL).
SQ SEQUENCE 306 AA: 32940 MW: E3532389BA9FC7C3 CRC64;

Query Match 1.8%; Score 7; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 DAGVDGL 191
|||||||
DB 185 DAGVDGL 191

Search completed: September 26, 2002, 08:36:28
Job time: 246 sec

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OM protein - protein search, using sw model

Run on: September 26, 2002, 08:32:01 ; Search time 28.49 seconds
(without alignments)
2331.697 Million cell updates/sec

Title: US-09-853-918-30
Perfect score: 384
Sequence: 1 MADYLISGGTGYVPEDGLTA.....MSAQIEGGVHGLSHYEKRLY 384

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SPTREMBL_19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	271	70.6	489	4 Q96NU2	Q96nu2 homo sapien
2	31	8.1	445	11 Q9DC16	Q9dc16 mus musculus
3	31	8.1	514	11 Q91Z11	Q91z11 mus musculus
4	21	5.5	521	3 Q9P8J2	Q9p8j2 candida alb
5	19	4.9	82	11 Q89058	Q89058 mus musculus
6	14	3.6	509	2 Q9RHG9	Q9rhg9 bacillus ce
7	14	3.6	509	2 Q9RHG1	Q9rhg1 bacillus ce
8	13	3.4	499	5 Q9GZH3	Q9gzh3 caenorhabdi
9	13	3.4	524	3 O14344	O14344 schizosacch
10	11	2.9	392	10 Q944T1	Q944t1 glycine max
11	11	2.9	502	10 Q9ZPA0	Q9zpa0 glycine max
12	10	2.6	165	4 Q96GP9	Q96gp9 homo sapien
13	10	2.6	485	16 Q9KGN8	Q9kgn8 bacillus ha
14	10	2.6	485	16 Q97FM8	Q97fm8 clostridium
15	10	2.6	501	10 Q9AY75	Q9ay75 oryza sativ
16	10	2.6	742	16 Q930X2	Q930x2 rhizobium m

17	9	2.3	116	10	O81282	O81282 prunus pers
18	9	2.3	232	3	P78758	P78758 schizosacch
19	9	2.3	392	2	Q92B97	Q92b97 rhodococcus
20	9	2.3	444	17	Q9YBU2	Q9ybu2 aeropyrum p
21	9	2.3	482	16	Q9X168	Q9x168 thermotoga
22	9	2.3	485	17	Q9HLK8	Q9hlk8 thermoplasma
23	9	2.3	485	17	Q978L4	Q978l4 thermoplasma
24	9	2.3	495	2	Q54171	Q54171 streptomyces
25	9	2.3	510	5	Q96387	Q96387 plasmodium
26	9	2.3	529	3	Q9UVL0	Q9uvl0 pneumocysti
27	9	2.3	1463	5	O44384	O44384 drosophila
28	9	2.3	63	5	Q9N9R9	Q9n9r9 leishmania
29	8	2.1	86	10	O41903	O41903 arabidopsis
30	8	2.1	157	3	O42831	O42831 saccharomyc
31	8	2.1	177	10	O942E0	O942e0 oryza sativ
32	8	2.1	208	16	Q97M06	Q97m06 clostridium
33	8	2.1	219	11	Q9D8A8	Q9d8a8 mus musculus
34	8	2.1	283	10	O81692	O81692 medicago sa
35	8	2.1	290	10	O43775	O43775 lycopersico
36	8	2.1	298	10	O49T3	O49t3 arabidopsis
37	8	2.1	302	10	Q9C9K7	Q9c9k7 arabidopsis
38	8	2.1	325	16	O92K22	O92k22 helicobacte
39	8	2.1	326	16	O05269	O05269 bacillus su
40	8	2.1	327	16	O25525	O25525 helicobacte
41	8	2.1	327	16	O99ZQ1	O99zq1 streptococc
42	8	2.1	327	16	Q97DK4	Q97dk4 clostridium
43	8	2.1	328	16	Q97OG5	Q97og5 streptococc
44	8	2.1	358	16	O92BX2	O92bx2 listeria in
45	8	2.1	364	17	Q9HRM3	Q9hrm3 halobacteri
46	8	2.1	367	10	Q39640	Q39640 cucurbita s
47	8	2.1	367	10	O944K6	O944k6 arabidopsis
48	8	2.1	368	10	O49506	O49506 arabidopsis
49	8	2.1	370	10	P93260	P93260 mesembryant
50	8	2.1	372	2	Q93N79	Q93n79 streptomyces
51	8	2.1	479	4	Q9UBD6	Q9ubd6 homo sapien
52	8	2.1	491	2	Q9ZGD9	Q9zgd9 streptomyces
53	8	2.1	500	16	Q92RT5	Q92rt5 rhizobium m
54	8	2.1	501	2	Q9L017	Q9l017 streptomyces
55	8	2.1	523	2	O86844	O86844 streptomyces
56	8	2.1	531	17	O972X2	O972x2 sulfolobus
57	8	2.1	594	16	O9RU24	O9ru24 deinococcus
58	8	2.1	700	11	Q9CXF5	Q9cxf5 mus musculus
59	8	2.1	1009	5	Q24749	Q24749 drosophila
60	7	1.8	37	5	Q9NAX5	Q9nax5 dictyosteli
61	7	1.8	60	5	Q9ULR4	Q9ulr4 caenorhabdi
62	7	1.8	90	11	P70443	P70443 mus musculus
63	7	1.8	91	16	O50688	O50688 borrelia bu
64	7	1.8	96	16	Q9JRX5	Q9jrx5 neisseria m
65	7	1.8	104	16	Q9K8A8	Q9k8a8 bacillus ha
66	7	1.8	114	16	Q9JS46	Q9js46 neisseria m
67	7	1.8	117	16	O9CBU0	O9cbu0 mycobacteri
68	7	1.8	130	2	Q9F8P8	Q9f8p8 carboxydoth
69	7	1.8	134	12	O73496	O73496 okra yellow
70	7	1.8	134	12	O91Z49	O91z49 bhendi yell
71	7	1.8	134	12	O99DR3	O99dr3 chilli leaf
72	7	1.8	135	16	O9PGJ5	O9pgj5 xyella fas
73	7	1.8	138	8	Q9C5F0	Q9c5f0 libellula q
74	7	1.8	140	16	O9ZJ49	O9zj49 helicobacte
75	7	1.8	143	10	Q94AR4	Q94ar4 arabidopsis
76	7	1.8	149	2	O68044	O68044 rhodobacter
77	7	1.8	153	10	Q9XF99	Q9xf99 medicago sa
78	7	1.8	154	10	O9FF72	O9ff72 arabidopsis
79	7	1.8	166	16	O9RU49	O9ru49 deinococcus
80	7	1.8	179	16	Q97I92	Q97i92 clostridium
81	7	1.8	197	2	Q9KXT6	Q9kxt6 streptomyces
82	7	1.8	211	10	O9SLP2	O9slp2 carica papa
83	7	1.8	217	10	Q9S7G0	Q9s7g0 arabidopsis
84	7	1.8	217	10	O94JX9	O94jx9 arabidopsis
85	7	1.8	217	16	O9ZK10	O9zk10 helicobacte
86	7	1.8	222	16	O9RXN1	O9rxn1 deinococcus
87	7	1.8	240	2	Q47310	Q47310 escherichia
88	7	1.8	240	11	Q9CSB1	Q9csb1 mus musculus
89	7	1.8	246	16	Q9Z912	Q9z912 chlamydia p

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90 049579 arabidopsis
91 023285 arabidopsis
92 023285 arabidopsis
93 092q20 oryza sativ
94 092q20 oryza sativ
95 092q20 oryza sativ
96 092q20 oryza sativ
97 092q20 oryza sativ
98 092q20 oryza sativ
99 092q20 oryza sativ
100 092q20 oryza sativ

RESULT 1
ID Q96NU2 PRELIMINARY; PRT; 489 AA.
AC Q96NU2;
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE CDNA FLJ30078 FIS CLONE BGG112000533, HIGHLY SIMILAR TO
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2 (EC 1.1.1.205).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Muraoka K., Kanehara K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RA "NEDO human cDNA sequencing project."
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK054640; BAB70780.1; -.
SQ SEQUENCE 489 AA; 52597 MW; 47A1273662A8C39B CRC64;

Query Match 70.6%; Score 271; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 4.6e-276;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 LLGAAAGTREDKYLRLDILTLQAGVDIVLDSQSGNSVYQIAMVHYIKQYPHLQVIGN 173
DB 219 LLGAAAGTREDKYLRLDILTLQAGVDIVLDSQSGNSVYQIAMVHYIKQYPHLQVIGN 278
QY 174 VVTAQAQNLIDAGVGLRVGMCGGCSICITQEVYMACRPGGTAVYKVAEYARRFGVPIIA 233
DB 279 VVTAQAQNLIDAGVGLRVGMCGGCSICITQEVYMACRPGGTAVYKVAEYARRFGVPIIA 338
QY 234 DGGITQTVGVHVKKALALGASVVMGSLAATTEAPGEYFFSDGVRLLKRYRGMGSLDAMEKS 293
DB 339 DGGITQTVGVHVKKALALGASVVMGSLAATTEAPGEYFFSDGVRLLKRYRGMGSLDAMEKS 398
QY 294 SSSOKRYFESGDKVKTAQGVSGSIQDKGSIQKQFVPLIAGIQHCCDIGARSLSVLRSM 353
DB 399 SSSOKRYFESGDKVKTAQGVSGSIQDKGSIQKQFVPLIAGIQHCCDIGARSLSVLRSM 458
QY 354 YSGELAFKRTMSAQEGGVHGLHSYEKRLY 384
DB 459 YSGELAFKRTMSAQEGGVHGLHSYEKRLY 489

RESULT 2
ID Q9DC16 PRELIMINARY; PRT; 445 AA.
AC Q9DC16;
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DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INOSINE 5'-PHOSPHATE DEHYDROGENASE 2.
GN IMPDH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Willing L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690 (2001).
DR EMBL: AK002676; BAB22278.1; -.
DR HSSP: P12268; 1B30.
DR MGD: MGI:109367; Impdh2.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART: SM00116; CBS; 2.
DR PROSITE: PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 445 AA; 48474 MW; 1B3A4006640CB4C9 CRC64;

Query Match 8.1%; Score 31; DB 11; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASVVMGSLAATTEAPGEYFFSDG 275
DB 306 KALALGASVVMGSLAATTEAPGEYFFSDG 336
QY 245 KALALGASVVMGSLAATTEAPGEYFFSDG 275
DB 306 KALALGASVVMGSLAATTEAPGEYFFSDG 336

RESULT 3
ID Q91211 PRELIMINARY; PRT; 514 AA.
AC Q91211;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE INOSINE 5'-PHOSPHATE DEHYDROGENASE 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010314; AAH10314.1; -.
```


SQ SEQUENCE 514 AA; 55815 MW; 17D25A5C5EBCC439 CRC64;

Query Match 8.1%; Score 31; DB 11; Length 514;

Best Local Similarity 100.0%; Pred. No. 1.5e-23; Mismatches 0; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGASTVMGMSLLAATTEAPGYFFSDG 275

|||||

Db 375 KALALGASTVMGMSLLAATTEAPGYFFSDG 405

RESULT 4

Q9P8J2

ID Q9P8J2 PRELIMINARY; PRT; 521 AA.

AC Q9P8J2;

DT 01-OCT-2000 (TRENBLrel. 15, Created)

DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)

DE PUTATIVE INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE.

GN IMH3.

OS Candida albicans (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCBI_TaxID=5476;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1006;

RX MEDLINE=20569171; PubMed=11119495;

RA Beckerman J., Chibana H., Turner J., Magee P.T.;

RT "Single-copy IMH3 allele is sufficient to confer resistance to

mycophenolic acid in Candida albicans and to mediate transformation of

clinical Candida species.";

RL Infect. Immun. 69:108-114.(2001).

DR EMBL; AF249293; AAF70813.1; -.

DR HSSP; P12268; 1B30.

DR InterPro; IPR000644; CBS.

DR InterPro; IPR003009; FMN_enzyme.

DR Pfam; PF00571; CBS; 2.

DR Pfam; PF00478; IMPDH_C; 1.

DR Pfam; PF01574; IMPDH_N; 1.

DR SMART; SM00116; CBS; 2.

DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.

FT VARIANT 47 47 V -> I.

FT VARIANT 102 102 A -> S.

FT VARIANT 400 400 D -> G.

SQ SEQUENCE 521 AA; 56267 MW; 7A1CF4DF6184FE7E CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 4.9e-13; Length 521;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GSICITQEVMACRPGQTAVY 218

|||||

Db 330 GSICITQEVMACRPGQTAVY 350

RESULT 5

O89058

ID O89058 PRELIMINARY; PRT; 82 AA.

AC O89058;

DT 01-NOV-1998 (TRENBLrel. 08, Created)

DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)

DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE 2 (FRAGMENT).

GN IMPDH2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE=99012997; PubMed=9798653;
RA Chu C.C., Paul W.E.;
RT "Expressed genes in interleukin-4 treated B cells identified by cDNA
representation difference analysis.";
RL MOL. Immunol. 35:487-502(1998).
DR EMBL; U89404; AAC36511.1; -.
DR HSSP; P12268; 1B30.
DR MGD; MGI:109367; Impdh2.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00478; IMPDH_C; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 8255 MW; 0ABA6BFD4FAB9964 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e-11; Length 82;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGNVVTAAQAKNLIDAGVD 189

|||||

Db 1 GGNVVTAAQAKNLIDAGVD 19

RESULT 6

Q9RHG9

ID Q9RHG9 PRELIMINARY; PRT; 509 AA.

AC Q9RHG9;

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)

DE IMP DEHYDROGENASE.

GN IMPDH.

OS Bacillus cereus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

OX NCBI_TaxID=1396;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TS-4;

RA Kim S., Miyamoto T., Honjoh K., Iio M., Hatanoto S.;

RT "Molecular cloning, overproduction and characterization of the

Bacillus cereus IMP dehydrogenase.";

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB035643; BAA88235.1; -.

DR HSSP; P50099; 1ZEF.

DR InterPro; IPR000644; CBS.

DR InterPro; IPR003009; FMN_enzyme.

DR InterPro; IPR001093; IMP_DH_GMP_RED.

DR Pfam; PF00571; CBS; 2.

DR Pfam; PF00478; IMPDH_C; 1.

DR Pfam; PF01574; IMPDH_N; 1.

DR SMART; SM00116; CBS; 2.

DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.

SQ SEQUENCE 509 AA; 55393 MW; 9E6ACB3872C4A451 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e-05; Length 509;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MDTVTADMAIAMA 83

|||||

Db 51 MDTVTADMAIAMA 64

RESULT 7

Q9RHG1

ID Q9RHG1 PRELIMINARY; PRT; 509 AA.

AC Q9RHL1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE IMPDH.
GN IMPDH.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 2152;
RA Kim S., Miyamoto T., Honjoh K., Iio M., Hatano S.;
RT "Molecular cloning, Overproduction and Characterization of the
RT Bacillus cereus";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB036795; BAA89464.1; -;
DR HSSP; P50099; IZFU.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 509 AA; 55194 MW; 77D0C58E2ED62D30 CRC64;

Query Match 3.6%; Score 14; DB 2; Length 509;
Best Local Similarity 100.0%; Pred. No. 1.le-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 MDTVTEADMAIAMA 83
Db 51 MDTVTEADMAIAMA 64
|||||

RESULT 8
Q9GZH3 PRELIMINARY; PRT; 499 AA.
AC Q9GZH3;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE T22D1.3 PROTEIN.
GN T22D1.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Geisel C., Bradshaw H., Hawkins M.;
RT "The sequence of C. elegans cosmid T22D1.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038052; AAF98635.1; -;
DR HSSP; P12266; 1B30.

DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 499 AA; 54298 MW; E96323563FE5D275 CRC64;

Query Match 3.4%; Score 13; DB 5; Length 499;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 LLAATTEAPGEYF 271
Db 395 LLAATTEAPGEYF 407
|||||

RESULT 9
O14344 PRELIMINARY; PRT; 524 AA.
AC O14344;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205)
DE (IMP DEHYDROGENASE) (IMPDH) (IMPD).
GN SPBC2F12.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: INOSINE 5'-PHOSPHATE + NAD(+) + H(2)O =
CC XANTHOSINE 5'-PHOSPHATE + NADH.
CC -1- PATHWAY: FIRST REACTION UNIQUE TO GMP BIOSYNTHESIS.
CC -1- SIMILARITY: TO OTHER EUKARYOTIC AND PROKARYOTIC IMPDH AND TO GMP
CC REDUCTASE.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
DR EMBL; Z97211; CAB10161.1; -;
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
KW Hypothetical protein; Oxidoreductase; NAD; GMP biosynthesis;
KW Purine biosynthesis; Multigene family; Repeat; CBS domain.
FT DOMAIN 119 174 CBS 1.
FT DOMAIN 182 236 CBS 2.
FT BINDING 337 337 IMP (POTENTIAL).
SQ SEQUENCE 524 AA; 57026 MW; E6C822C2E74674F CRC64;

Query Match 3.4%; Score 13; DB 3; Length 524;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 CITQEVNACGRPQ 213
Db 337 CITQEVNACGRPQ 349
|||||

RESULT 10

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Q944T1
ID Q944T1 PRELIMINARY; PRT; 392 AA.
AC 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE-LIKE PROTEIN (FRAGMENT).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ROOT TIP;
RA Enclayev V., Weschke W., Manteuffel R.;
RT "Study of Gene Expression in Soybean under Aluminium Stress
Conditions.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF421559; AAL18815.1; -.
FT NON_TER 1
SQ SEQUENCE 392 AA; 41872 MW; 9FAD1A0DC5A8BC17 CRC64;

Query Match 2.9%; Score 11; DB 10; Length 392;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GAAVGTREDDK 127
Db 126 GAAVGTREDDK 136

RESULT 11
Q92PA0 PRELIMINARY; PRT; 502 AA.
AC Q92PA0;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INOSINE MONOPHOSPHATE DEHYDROGENASE.
GN IMPDH1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RA Cao Y., Schubert K.R.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ010201; CAB38030.1; -.
DR HSSP; P12268; 1B30.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 502 AA; 53407 MW; 617AB87613C36AA4 CRC64;

Query Match 2.9%; Score 11; DB 10; Length 502;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 GAAVGTREDDK 127
Db 237 GAAVGTREDDK 247

RESULT 12
Q96GP9 PRELIMINARY; PRT; 165 AA.
ID Q96GP9

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AC Q96GP9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:16650).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE, AND RHABDOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009321; AAH09321.1; -.
SQ SEQUENCE 165 AA; 17677 MW; 4E47B26D55121D80 CRC64;

Query Match 2.6%; Score 10; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADYLIISGCT 10
Db 71 MADYLIISGCT 80

RESULT 13
Q9KGN8 PRELIMINARY; PRT; 485 AA.
AC Q9KGN8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE INOSITOL-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.205).
GN GUAB OR BH0020.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001507; BAB03739.1; -.
DR HSSP; P50099; 12FJ.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Oxidoreductase; Complete proteome.
SQ SEQUENCE 485 AA; 52429 MW; D0B64489E5CF8B60 CRC64;

Query Match 2.6%; Score 10; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPITADGGI 237
Db 333 GVPITADGGI 342

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RESULT 14
Q97FM8 ID Q97FM8 PRELIMINARY; PRT; 485 AA.
AC Q97FM8;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IMP DEHYDROGENASE.
GN CAC2701.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusev R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007768; AAK80847.1; -
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 485 AA; 52188 MW; 994D1C5347F7A267 CRC64;

Query Match 2.6%; Score 10; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 GVPIADGGI 237
Db 331 GVPIADGGI 340
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RESULT 15
Q9AY75 ID Q9AY75 PRELIMINARY; PRT; 501 AA.
AC Q9AY75;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE INOSINE MONOPHOSPHATE DEHYDROGENASE.
GN OSJNBA0091J19.1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONARE;
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSJNBA0091J19 genomic sequence."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC084320; AAK09225.1; -
DR HSSP; P12268; 1B30.
DR InterPro: IPR000644; CBS.
DR InterPro: IPR003009; FMN_enzyme.
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DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 1.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 501 AA; 52655 MW; DDE295CB714C3802 CRC64;

Query Match 2.6%; Score 10; DB 10; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 GVDGLRVGMG 196
Db 306 GVDGLRVGMG 315
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RESULT 16
Q930X2 ID Q930X2 PRELIMINARY; PRT; 742 AA.
AC Q930X2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE KINASE/ESTERASE.
GN SMA0137.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacterium; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021.
RX MEDLINE=21396509; PubMed=11481432;
RA Barrett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA Barclay-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT "Nucleotide sequence and predicted functions of the entire
RT Sinorhizobium meliloti pSyma megaplasmid."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
DR EMBL: AE007201; AAK64730.1; -
KW Kinase; Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 742 AA; 81351 MW; B31AD546F5E81904 CRC64;

Query Match 2.6%; Score 10; DB 16; Length 742;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 ATAMALMGGI 88
Db 27 ATAMALMGGI 36
|||||
|

RESULT 17
O81282 ID O81282 PRELIMINARY; PRT; 116 AA.
AC O81282;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (FRAGMENT).
OS Prunus persica (peach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=3760;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. FEICHENG;
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RA Ma Q.H.;
RT "Cloning and analysis of a cDNA coding for inosin monophosphatase
RT dehydrogenase from peach.";
RL J. Plant Physiol. 156:130-132(2000).
DR EMBL; AF068844; RAC19381.1; -.
DR HSSP; P12268; 1B30.
FT NON_TER 1
SQ SEQUENCE 116 AA; 12394 MW; 23FB6F32649DD12D CRC64;

Query Match 2.3%; Score 9; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 KKYRGMGSL 287
Db 13 KKYRGMGSL 21
|||||
|

RESULT 18
P78758 ID P78758 PRELIMINARY; PRT; 232 AA.
AC P78758;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN PROTEIN (FRAGMENT).
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR745;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT "Identification of open reading frames in Schizosaccharomyces pombe
RT cDNAs.";
RL DNA Res. 4:363-369(1997).
DR EMBL; D89106; BAAL3769.1; -.
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 25376 MW; 1DE04232ED077A97 CRC64;

Query Match 2.3%; Score 9; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDIVTE 75
Db 13 SSPMDIVTE 21
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|

RESULT 19
Q92B97 ID Q92B97 PRELIMINARY; PRT; 392 AA.
AC Q92B97;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 41.6 KDA PROTEIN.
OS Rhodococcus erythropolis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=1833;

Ma Q.H.;
RT "Cloning and analysis of a cDNA coding for inosin monophosphatase
RT dehydrogenase from peach.";
RL J. Plant Physiol. 156:130-132(2000).
DR EMBL; AF068844; RAC19381.1; -.
DR HSSP; P12268; 1B30.
FT NON_TER 1
SQ SEQUENCE 116 AA; 12394 MW; 23FB6F32649DD12D CRC64;

Query Match 2.3%; Score 9; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 279 KKYRGMGSL 287
Db 13 KKYRGMGSL 21
|||||
|

RESULT 18
P78758 ID P78758 PRELIMINARY; PRT; 232 AA.
AC P78758;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN PROTEIN (FRAGMENT).
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PR745;
RX MEDLINE=98162722; PubMed=9501991;
RA Yoshioka S., Kato K., Nakai K., Okayama H., Nojima H.;
RT "Identification of open reading frames in Schizosaccharomyces pombe
RT cDNAs.";
RL DNA Res. 4:363-369(1997).
DR EMBL; D89106; BAAL3769.1; -.
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
FT NON_TER 1
FT NON_TER 232
SQ SEQUENCE 232 AA; 25376 MW; 1DE04232ED077A97 CRC64;

Query Match 2.3%; Score 9; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDIVTE 75
Db 13 SSPMDIVTE 21
|||||
|

RESULT 19
Q92B97 ID Q92B97 PRELIMINARY; PRT; 392 AA.
AC Q92B97;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 41.6 KDA PROTEIN.
OS Rhodococcus erythropolis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=1833;


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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NI86/21;
RX MEDLINE=94349216; PubMed=8069783;
RA de Mot R., Nagy I., Schoofs G., Vanderleyden J.;
RT "Sequence of Rhodococcus gene cluster encoding the subunits of
RT ethanolamine ammonia-lyase and an APC-like permease.";
RL Can. J. Microbiol. 40:403-407(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NI86/21;
RX MEDLINE=95138028; PubMed=7836301;
RA Nagy I., Schoofs G., Compennolle F., Proost P., Vanderleyden J.,
RA de Mot R.;
RT "Degradation of the thiocarbamate herbicide EPTC (S-ethyl
RT dipropylcarbamothioate) and biosafening by Rhodococcus sp. strain
RT NI86/21 involve an inducible cytochrome P-450 system and aldehyde
RT dehydrogenase.";
RL J. Bacteriol. 177:676-687(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NI86/21;
RX MEDLINE=20029277; PubMed=10565547;
RA Nagy I., De Mot R.;
RT "Sequence analysis of the oxidase/reductase genes upstream of the
RT Rhodococcus erythropolis aldehyde dehydrogenase gene thcA reveals a
RT gene organization different from Mycobacterium tuberculosis.";
RL DNA Seq. 10:61-66(1999).
DR EMBL; U17129; AAC77479.1; -.
DR HSSP; P05414; 1AL8.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR00262; FMN_hydroxy_acid_dh.
DR Pfam; PF01070; FMN_dh; 1.
KW Hypothetical protein.
SQ SEQUENCE 392 AA; 41597 MW; BD2EBC25F20F36AB CRC64;

Query Match 2.3%; Score 9; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 VVKALALGA 251
Db 319 VVKALALGA 327
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|

RESULT 20
Q9YBU2 ID Q9YBU2 PRELIMINARY; PRT; 444 AA.
AC Q9YBU2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 444AA LONG HYPOTHETICAL IMP DEHYDROGENASE.
GN APEI507.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae;
OC Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kwarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000061; BAA80506.1; -.


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DR HSSP; P12268; 1B30.
DR InterPro; IPR001295; DHO_dh.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR PROSITE; PS00912; DHODEHASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 444 AA; 47215 MW; 4E3C1C942936905A CRC64;

Query Match      2.3%; Score 9; DB 17; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTE 75
Db 62 SSPMDTVTE 70

RESULT 21
Q9X168 PRELIMINARY; PRT; 482 AA.
AC Q9X168;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
GN TW1347.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001789; AAD36418.1; -.
DR HSSP; P12268; 1B30.
DR TIGR; TW1347; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 482 AA; 52014 MW; 4E08237F69D909FA CRC64;

Query Match      2.3%; Score 9; DB 16; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 VPIADGGI 237
Db 329 VPIADGGI 337

RESULT 22
Q9HLK8 PRELIMINARY; PRT; 485 AA.
ID Q9HLK8
AC Q9HLK8;

Query Match      2.3%; Score 9; DB 16; Length 482;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 VPIADGGI 237
Db 329 VPIADGGI 337

RESULT 22
Q9HLK8 PRELIMINARY; PRT; 485 AA.
ID Q9HLK8
AC Q9HLK8;

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
GN TA0219.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmataceae;
OC Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frisman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
DR EMBL; AL445063; CAC11365.1; -.
DR HSSP; P49058; 1EEP.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 485 AA; 52225 MW; 4450C3DC8FA68673 CRC64;

Query Match      2.3%; Score 9; DB 17; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 67 SSPMDTVTE 75
Db 50 SSPMDTVTE 58

RESULT 23
Q978L4 PRELIMINARY; PRT; 485 AA.
ID Q978L4
AC Q978L4;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IMP DEHYDROGENASE.
GN TVG1445839.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmataceae;
OC Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSSI / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima T., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
DR EMBL; AF000996; BAB60543.1; -.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.

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DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
KW Complete proteome.
SQ SEQUENCE 485 AA; 52726 MW; 7919D260618917AF CRC64;

Query Match 2.3%; Score 9; DB 17; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SSPMDTVTE 75
|||||

Db 50 SSPMDTVTE 58

RESULT 24
Q54171 PRELIMINARY; PRT; 495 AA.

AC Q54171;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PUTATIVE OXYGENASE.
GN URDE.
OS Streptomyces fradiae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1906;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUE2717;
RX MEDLINE=96042088; PubMed=7592377;
RA Decker H., Haag S.;
RT "Cloning and characterization of a polyketide synthase from
Streptomyces fradiae TUE2717 encoding the genes for biosynthesis of
the angucycline antibiotic urdamycin A and a gene probably involved in
its oxygenation.";
RL J. Bacteriol. 177:6126-6136(1995).
DR EMBL; X87093; CAA60567.1; -;
DR InterPro; IPR000733; flavo_monooxygenase.
DR InterPro; IPR002938; Moxv_FAD_binding.
DR InterPro; IPR000205; NAD_binding.
DR InterPro; IPR003042; Rng_monooxygenase.
DR Pfam; PF01494; FAD_binding_3; 1.
DR Pfam; PF01360; Monooxygenase; 1.
DR PRINTS; PR00420; RNMGNXGNASE.
SQ SEQUENCE 495 AA; 53399 MW; 0F7B9A373A27B700 CRC64;

Query Match 2.3%; Score 9; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 AGVDVIVLD 144
|||||

Db 24 AGVDVIVLD 32

RESULT 25
Q96387 PRELIMINARY; PRT; 510 AA.

AC Q96387;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Prosise G.L., James A.A., Luecke H.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF035679; AAD10256.1; -;
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 510 AA; 56148 MW; 449413AD3E41A7D0 CRC64;

Query Match 2.3%; Score 9; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 66 ISSPMDTVT 74
|||||

Db 53 ISSPMDTVT 61

RESULT 26

Q9UVL0 PRELIMINARY; PRT; 529 AA.

AC Q9UVL0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE.
OS Pneumocystis carinii.
OC Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC Pneumocystis.
OX NCBI_TaxID=4754;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21125226; PubMed=112323253;
RA Ye D., Lee C.H., Queener S.F.;
RT "Differential splicing of Pneumocystis carinii f. sp. carinii inosine
5'-monophosphate dehydrogenase pre-mRNA.";
RL Gene 263:151-158(2001).
DR EMBL; AF196975; AAF13230.1; -;
DR HSSP; P12268; 1B30.
DR InterPro; IPR000644; CBS.
DR InterPro; IPR003009; FMN_enzyme.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00478; IMPDH_C; 1.
DR Pfam; PF01574; IMPDH_N; 1.
DR SMART; SM00116; CBS; 2.
DR PROSITE; PS00487; IMP_DH_GMP_RED; 1.
SQ SEQUENCE 529 AA; 58066 MW; 030573A8854ADB5A CRC64;

Query Match 2.3%; Score 9; DB 3; Length 529;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 67 SSPMDTVTE 75
|||||

Db 77 SSPMDTVTE 85

RESULT 27

O44384 PRELIMINARY; PRT; 1463 AA.

ID O44384;
AC O44384;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE PRGAG-POL.
GN GYPSY\POL OR GAG-POL.
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Petropoulos C.J.;
RL (in) Coffin J.M. (eds.);
RL Retroviruses, pp.757-757, Cold Spring Harbor Laboratory Press,
RL New York (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Chappey C.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF033821; AAC82604.1; -
DR FlyBase; FBgn0014966; gypsy\pol.
DR InterPro; IPR0011995; Asp_prot_retrov.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR000477; Rvtse.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00077; rvp; 1.
DR Pfam; PF00078; rvt; 1.
KW RNA-directed DNA polymerase.
FT CHAIN 1 843
FT CHAIN 844 1463 PR-RT-RH-IN.
SQ SEQUENCE 1463 AA; 166015 MW; 1A63F7909092E2C7 CRC64;

Query Match 2.3%; Score 9; DB 5; Length 1463;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 LDLLTQAGV 138
Db 522 LDLLTQAGV 530
|||||

RESULT 28
Q9N9R9 ID Q9N9R9 PRELIMINARY; PRT; 63 AA.
AC Q9N9R9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (FRAGMENT).
GN L2185.10.
OS Leishmania major.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RA Bothe G., Pohl T., Ivens A.C., Quail M., Rajandream M.A.,
RA Barrell B.G.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIEDLIN;
RX MEDLINE=98146435; PubMed=9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL; AL358712; CAB94117.2; -
DR HSSP; P12268; 1B30.
DR InterPro; IPR001053; IMP_DH_GMP_RED.
DR Pfam; PF01574; IMPDH_N; 1.
FT NON_TER 63 63
SQ SEQUENCE 63 AA; 7048 MW; 2315405AF9B78404 CRC64;

Query Match 2.1%; Score 8; DB 5; Length 63;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 DGLTYNDF 35
Db 26 DGLTYNDF 33
|||||

RESULT 29
Q41903 ID Q41903 PRELIMINARY; PRT; 86 AA.
AC Q41903;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (S)-2-HYDROXY-ACID OXIDASE (FRAGMENT).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-GREEN SILIQUES OF A THALIANA ECOTYPE COLUMBIA;
RA Raynal M., Greillett F., Laudie M., Meyer Y., Cooke R., Delsen M.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z17593; CAA79007.1; -
DR HSSP; P05414; IGOX.
DR InterPro; IPR003009; FMN_enzyme.
FT NON_TER 1 1
SQ SEQUENCE 86 AA; 9420 MW; 452D0A8729FCD727 CRC64;

Query Match 2.1%; Score 8; DB 10; Length 86;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
Db 15 KALALGAS 22
|||||

RESULT 30
O42831 ID O42831 PRELIMINARY; PRT; 157 AA.
AC O42831;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE YAR075WP.
GN YAR075W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=81198945; PubMed=7015287;
RA Page G.S., Hall B.D.;
RT "Characterization of the yeast tRNA Ser genomic organization and DNA
sequence.";
RL Nucleic Acids Res. 9:921-934(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=84207870; PubMed=6327259;
RA Eigel A., Feldmann H.;
RT "Tyl and delta elements occur adjacent to several tRNA genes in
RT yeast.";
RL EMBO J. 1:1245-1250(1982).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;

RX MEDLINE=83168913; PubMed=6300772;
RA Arima K., Oshima T., Kubota I., Nakamura N., Mizunaga T., Toh-E A.;
RT "The nucleotide sequence of the yeast PHO5 gene: a putative precursor
of repressible acid phosphatase contains a signal peptide.";
RL Nucleic Acids Res. 11:1657-1672(1983).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=84026507; PubMed=6194896;
RA Baldi M.I., Mattoccia E., Tocchini-Valentini G.P.;
RT "Role of RNA structure in splicing: excision of the intervening
sequence in yeast tRNA^{3leu} is dependent on the formation of a D
stem.";
RL Cell 35:109-115(1983).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=88087281; PubMed=2447089;
RA Clark D.J., Blanchone V.W., Haywood L.J., Dildine S.L.,
RA Sandmeyer S.B.;
RT "A yeast sigma composite element, TX3, has properties of a
retrotransposon.";
RL J. Biol. Chem. 263:1413-1423(1988).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=90203022; PubMed=1969416;
RA Natsumeda Y., Ohno S., Kawasaki H., Konno Y., Weber G., Suzuki K.;
RT "Two distinct cDNAs for human IMP dehydrogenase.";
RL J. Biol. Chem. 265:5292-5295(1990).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=90158830; PubMed=2137557;
RA Lux S.E., John K.M., Bennett V.;
RT "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated
structure with homology to tissue-differentiation and cell-cycle
control proteins.";
RL Nature 344:36-42(1990).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=90243258; PubMed=1574125;
RA Levanon D., Hsieh C.L., Francke U., Dawson P.A., Ridgway N.D.,
RA Brown M.S., Goldstein J.L.;
RT "cDNA cloning of human oxysterol-binding protein and localization of
the gene to human chromosome 11 and mouse chromosome 19.";
RL Genomics 7:65-74(1990).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=92244356; PubMed=1574125;
RA Oliver S.G., Van der Aart O.J., Agostoni-Carbone M.L., Aigle M.,
RA Alberghina L., Alexandraki D., Antoine G., Anwar R., Ballesta J.P.,
RA Benit P.;
RT "The complete DNA sequence of yeast chromosome III.";
RL Nature 357:38-46(1992).
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=92254505; PubMed=1580102;
RA Biteau N., Fremaux C., Hebrard S., Menara A., Aigle M., Crouzet M.;
RT "The complete sequence of a 10.8kb fragment to the right of the
chromosome III centromere of *Saccharomyces cerevisiae*.";
RL Yeast 8:61-70(1992).
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=93289821; PubMed=8511970;
RA Teunissen A.W., Holub E., van der Hucht J., van den Berg J.A.,
RA Steensma H.Y.;
RT "Sequence of the open reading frame of the FLO1 gene from
Saccharomyces cerevisiae.";

RL Yeast 9:423-427(1993).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=95028152; PubMed=7941740;
RA Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
RA Delaney S., Ouellette B.F., Barton A.B., Kaback D.B.;
RT "Sequencing of chromosome I of *Saccharomyces cerevisiae*: analysis of
the 42 kbp SPO7-CEN1-CDC15 region.";
RL Yeast 10:535-541(1994).
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RX MEDLINE=94287711; PubMed=8017104;
RA Jiang B., Brown J.L., Sheraton J., Fortin N., Bussey H.;
RT "A new family of yeast genes implicated in ergosterol synthesis is
related to the human oxysterol binding protein.";
RL Yeast 10:341-353(1994).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RA Schmalix W.A., Bandlow W.;
RT Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RA Volckaert G., Valle G.;
RT Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [16]
RP SEQUENCE OF 13-157 FROM N.A.
RC STRAIN=S288C/AB972;
RA Zhong W., Louis E.J., Bussey H.;
RT Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
RN [17]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C/AB972;
RA Bussey H., Keng T., Storms R.K., Vo D., Zhong W., Fortin N.,
RA Barton A.B., Kaback D.B., Clark M.W.;
RT Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; L28920; AAC09511.1; -
DR HSP; P12268; I830
DR SGD; S0002145; YAR075W.
DR InterPro; IPR001093; IMP_DH_GMP_RED.
DR Pfam; PF00478; IMPDH_C; 1.
SQ SEQUENCE 157 AA; 17003 MW; 90F3FCF03C244FCF CRC64;

Query Match 2.1%; Score 8; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 376 LHSYEKRL 383
DB 148 LHSYEKRL 155
|||||

RESULT 31
Q942E0 PRELIMINARY; PRT; 177 AA.
AC Q942E0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P0480C01.26 PROTEIN.
GN P0480C01.26.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RL clone:PO480C01.";
 DR Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 SQ EMBL: AP003453; BAB68066.1; -; -;
 SEQUENCE 177 AA; 19066 MW; 0EFD31AC74D2608A CRC64;

Query Match 2.1%; Score 8; DB 10; Length 177;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 TPLISSPM 70
 Db 168 TPLISSPM 175
 |||||

RESULT 32
 Q97M06

ID . Q97M06 PRELIMINARY; PRT; 208 AA.
 AC Q97M06;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DEOXYPHOSPHOGLUCONATE ALDOLASE (GENE KAGA).
 GN CAC0394.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Olu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum.";
 RL J. Bacteriol. 183:4823-4838(2001).
 DR EMBL: AS007554; AAK78374.1; -;
 DR InterPro: IPR000887; Aldise_KDPC_KHG.
 DR Pfam: PF01081; Aldolase; 1.
 KW Complete proteome.
 SQ SEQUENCE 208 AA; 22457 MW; 15BA9819C74B8346 CRC64;

Query Match 2.1%; Score 8; DB 16; Length 208;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 VVTAQAQK 181
 Db 71 VVTAQAQK 78
 |||||

RESULT 33
 Q9D8A8

ID Q9D8A8 PRELIMINARY; PRT; 219 AA.
 AC Q9D8A8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE 4432405804RIK PROTEIN.
 GN 4432405804RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;

RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Donato M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK008223; BAB25541.1; -;
 DR MGD: MGI:1915228; 4432405B04RIK
 SQ SEQUENCE 219 AA; 24205 MW; 1775AD520CCE2892 CRC64;

Query Match 2.1%; Score 8; DB 11; Length 219;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 RLDLLTQA 136
 Db 55 RLDLLTQA 62
 |||||

RESULT 34
 O81692

ID O81692 PRELIMINARY; PRT; 283 AA.
 AC O81692;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE GLYCOLATE OXIDASE (FRAGMENT).
 OS Medicago sativa (Alfalfa).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
 OX NCBI_TaxID=3879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SHOOT APICAL MERISTEM;
 RA Stout J.M., McKersie B.D.;
 RT "Gene expression in alfalfa.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF082874; AAC32392.1; -;
 DR HSSP: P05414; 1AL8.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR00262; FMN_hydroxy_acid_dh.
 DR Pfam: PF01070; FMN_dh; 1.
 FT NON_TER 1
 SQ SEQUENCE 283 AA; 30550 MW; F701D54D3B5F56D9 CRC64;

Query Match 2.1%; Score 8; DB 10; Length 283;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 KALALGAS 252
 Db 208 KALALGAS 215
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RESULT 35

Q43775
 ID AC Q43775 PRELIMINARY; PRT; 290 AA.
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE GLYCULATE OXIDASE (EC 1.1.3.15) (FRAGMENT).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. BREEDING LINE 'DE RUITER 83G38'; TISSUE=LEAF;
 RA Gilpin B.J., Leung D.W., Lancaster J.E.;
 RT "Nucleotide sequence of a nuclear clone of alliinase (Accession No.
 L48614) from onion (PGR95-125).";
 RL Plant Physiol. 110:336-336(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. BREEDING LINE 'DE RUITER 83G38'; TISSUE=LEAF;
 RA Speirs J.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X92888; CAA63482.1; -;
 DR HSSP; P05414; 1AL8.
 DR InterPro; IPR003009; FMN_enzyme.
 DR Pfam; PF01070; FMN_dh; 1.
 DR PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.
 KW OXIDOREDUCTASE.
 FT NON_TER 1
 SQ SEQUENCE 290 AA; 31297 MW; 3DC9E093DBF75AB5 CRC64;
 Query Match 2.1%; Score 8; DB 10; Length 290;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 KALALGAS 252
 DB 216 KALALGAS 223
 RESULT 36
 Q949T3
 ID Q949T3 PRELIMINARY; PRT; 298 AA.
 AC Q949T3;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PUTATIVE GLYCULATE OXIDASE.
 GN AT4G18360
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
 RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kaniwa A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
 RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Shinn P.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
 RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene AT4G18360 (GI:7268629).";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY050902; AAK93579.1; -;
 SQ SEQUENCE 298 AA; 32308 MW; C16A3E6E80A5AE15 CRC64;

Q43775
 ID AC Q43775 PRELIMINARY; PRT; 290 AA.
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE GLYCULATE OXIDASE (EC 1.1.3.15) (FRAGMENT).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. BREEDING LINE 'DE RUITER 83G38'; TISSUE=LEAF;
 RA Gilpin B.J., Leung D.W., Lancaster J.E.;
 RT "Nucleotide sequence of a nuclear clone of alliinase (Accession No.
 L48614) from onion (PGR95-125).";
 RL Plant Physiol. 110:336-336(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. BREEDING LINE 'DE RUITER 83G38'; TISSUE=LEAF;
 RA Speirs J.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X92888; CAA63482.1; -;
 DR HSSP; P05414; 1AL8.
 DR InterPro; IPR003009; FMN_enzyme.
 DR Pfam; PF01070; FMN_dh; 1.
 DR PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.
 KW OXIDOREDUCTASE.
 FT NON_TER 1
 SQ SEQUENCE 290 AA; 31297 MW; 3DC9E093DBF75AB5 CRC64;
 Query Match 2.1%; Score 8; DB 10; Length 290;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 245 KALALGAS 252
 DB 216 KALALGAS 223
 RESULT 36
 Q949T3
 ID Q949T3 PRELIMINARY; PRT; 298 AA.
 AC Q949T3;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE PUTATIVE GLYCULATE OXIDASE.
 GN AT4G18360
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,
 RA Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
 RA Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kaniwa A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
 RA Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Shinn P.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
 RA Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene AT4G18360 (GI:7268629).";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY050902; AAK93579.1; -;
 SQ SEQUENCE 298 AA; 32308 MW; C16A3E6E80A5AE15 CRC64;

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OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
RL EMBL: AE001509; AAD06382.1; -.
DR HSSP: P12268; 1B30.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
KW Complete proteome.
SQ SEQUENCE 325 AA; 35845 MW; 86F1FCF53DE69E91 CRC64;

Query Match 2.1%; Score 8; DB 16; Length 325;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237
DB 202 PIIADGGI 209

RESULT 39
O05269
ID O05269 PRELIMINARY; PRT; 326 AA.
AC O05269;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HYPOTHETICAL 35.8 KDA PROTEIN.
GN YUMD.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Oudega B., Koningssteyn G., Ramon-De Haan M., Rodrigues L.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connercon I.F., Cummings N.J., Daniel R.A.,
RA Denzlot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Neone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

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RA Parro V., Pohl T.M., Portetelle D., Porvollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
RL [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z93939; CAB07955.1; -.
DR EMBL: Z99120; CAB15203.1; -.
DR HSSP: P12268; 1B30.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.
DR Pfam: PF00478; IMPDH_C; 1.
DR Pfam: PF01574; IMPDH_N; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 326 AA; 35819 MW; 4D5EC6F22951D353 CRC64;

Query Match 2.1%; Score 8; DB 16; Length 326;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 230 PIIADGGI 237
DB 203 PIIADGGI 210

RESULT 40
O25525
ID O25525 PRELIMINARY; PRT; 327 AA.
AC O25525;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GMP REDUCTASE (GUNC).
GN HP0854.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
RL EMBL: AE000596; AAD07901.1; -.
DR HSSP: P12268; 1B30.
DR TIGR: HP0854; -.
DR InterPro: IPR003009; FMN_enzyme.
DR InterPro: IPR001093; IMP_DH_GMP_RED.

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DR Pfam: PF00478; IMPDH_C; 1.
 DR Pfam: PF01574; IMPDH_N; 1.
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 327 AA; 36038 MW; E9ED3053C3E103C8 CRC64;

Query Match 2.18; Score 8; DB 16; Length 327;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 230 PIIADGGI 237
 Db 204 PIIADGGI 211

Search completed: September 26, 2002, 08:36:09
 Job time: 248 sec

